

**RNA INTERFERENCE MEDIATED INHIBITION OF VASCULAR
 ENDOTHELIAL GROWTH FACTOR AND VASCULAR ENDOTHELIAL
 GROWTH FACTOR RECEPTOR GENE EXPRESSION USING SHORT
 INTERFERING NUCLEIC ACID (siNA)**

5 This invention is a continuation-in-part of McSwiggen, PCT/US03/05022, filed
 February 20, 2003, which claims the benefit of Beigelman USSN 60/358,580 filed
 February 20, 2002, of Beigelman USSN 60/363,124 filed March 11, 2002, of Beigelman
 USSN 60/386,782 filed June 6, 2002, of McSwiggen, USSN 60/393,796 filed July 3,
 2002, of McSwiggen, USSN 60/399,348 filed July 29, 2002, of Beigelman USSN
 10 60/406,784 filed August 29, 2002, of Beigelman USSN 60/408,378 filed September 5,
 2002, of Beigelman USSN 60/409,293 filed September 9, 2002, and of Beigelman USSN
 60/440,129 filed January 15, 2003, and which is a continuation-in-part of Pavco, USSN
 10/306,747, filed November 27, 2002, which claims the benefit of Pavco USSN
 60/334461, filed November 30, 2001, a continuation-in-part of Pavco, USSN 10/287,949
 15 filed November 4, 2002, and a continuation-in-part of Pavco, PCT/US02/17674 filed
 May 29, 2002. The instant application claims priority to all of the listed applications,
 which are hereby incorporated by reference herein in their entireties, including the
 drawings.

Field Of The Invention

20 The present invention concerns compounds, compositions, and methods for the
 study, diagnosis, and treatment of conditions and diseases that respond to the modulation
 of vascular endothelial growth factor (VEGF) and/or vascular endothelial growth factor
 receptor (e.g., VEGFr1, VEGFr2 and/or VEGFr3) gene expression and/or activity. The
 present invention also concerns compounds, compositions, and methods relating to
 25 conditions and diseases that respond to the modulation of expression and/or activity of
 genes involved in VEGF and VEGF receptor pathways. Specifically, the invention
 relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA),
 short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA),
 and short hairpin RNA (shRNA) molecules capable of mediating RNA interference
 30 (RNAi) against VEGF and VEGF receptor gene expression.

Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understanding of the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention.

5 RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806; Hamilton *et al.*, 1999, *Science*, 286, 950-951). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of
10 post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random
15 integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-
20 oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Hamilton *et al.*, *supra*;
25 Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Hamilton *et al.*, *supra*; Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in
30 translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having

sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Bahramian and Zarbl, 1999, *Molecular and Cellular Biology*, 19, 274-283 and Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mammalian systems. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). In addition, Elbashir *et al.*, *supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely

abolishes RNAi activity. Li *et al.*, International PCT Publication No. WO 00/44914, and Beach *et al.*, International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in siRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, tested certain chemical modifications targeting the *unc-22* gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified bases also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi
5 system and the use of specific siRNA molecules for certain functional genomic and certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO 00/44914, describe the use of specific dsRNAs for attenuating the expression of certain
10 target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian cells using certain dsRNA molecules. Fire *et al.*, International PCT Publication No. WO 99/32619, describe particular methods for introducing certain dsRNA molecules into cells for use in inhibiting gene expression. Plaetinck *et al.*, International PCT
15 Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific dsRNA molecules. Mello *et al.*, International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.*, International PCT Publication No. WO 99/07409, describe specific
20 compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse *et al.*, International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll *et al.*, International PCT Publication No. WO 01/49844, describe specific DNA constructs for use in facilitating gene silencing in targeted
25 organisms.

Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, describe specific chemically-modified siRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb
30 gene expression in plants using certain dsRNAs. Churikov *et al.*, International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.*, International PCT Publication No. WO 01/53475, describe certain methods for isolating a *Neurospora*

silencing gene and uses thereof. Reed *et al.*, International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.*, International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak *et al.*, International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.*, International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.*, International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk *et al.*, International PCT Publication No. WO 00/63364, and Satishchandran *et al.*, International PCT Publication No. WO 01/04313, describe certain methods and compositions for inhibiting the function of certain polynucleotide sequences using certain dsRNAs. Echeverri *et al.*, International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.*, International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using RNAi. Graham *et al.*, International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.*, US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain long dsRNA (greater than 25 nucleotide) constructs that mediate RNAi. Harborth *et al.*, 2003, Antisense & Nucleic Acid Drug Development, 13, 83-105, describe certain chemically and structurally modified siRNA molecules. Chiu and Rana, 2003, RNA, 9, 1034-1048, describe certain chemically and structurally modified siRNA molecules.

SUMMARY OF THE INVENTION

This invention relates to compounds, compositions, and methods useful for modulating the expression of genes, such as those genes associated with angiogenesis and proliferation, using short interfering nucleic acid (siNA) molecules. This invention also relates to compounds, compositions, and methods useful for modulating the expression and activity of vascular endothelial growth factor (VEGF) and/or vascular endothelial growth factor receptor (e.g., VEGFr1, VEGFr2, VEGFr3) genes, or genes involved in VEGF and/or VEGFr pathways of gene expression and/or VEGF activity by RNA interference (RNAi) using small nucleic acid molecules. In particular, the instant

invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of VEGF and/or VEGFr genes. A siNA of the invention can be unmodified
 5 or chemically-modified. A siNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-modified synthetic short interfering nucleic acid (siNA) molecules capable of modulating VEGF and/or VEGFr gene expression or activity in cells by RNA interference (RNAi). The use of chemically-modified siNA improves
 10 various properties of native siNA molecules through increased resistance to nuclease degradation *in vivo* and/or through improved cellular uptake. Further, contrary to earlier published studies, siNA having multiple chemical modifications retains its RNAi activity. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, target validation, genomic discovery,
 15 genetic engineering, and pharmacogenomic applications.

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of gene(s) encoding proteins, such as vascular endothelial growth factor (VEGF) and/or vascular endothelial growth factor receptors (e.g., VEGFr1, VEGFr2, VEGFr3), associated with
 20 the maintenance and/or development of cancer and other proliferative diseases, such as genes encoding sequences comprising those sequences referred to by GenBank Accession Nos. shown in **Table I**, referred to herein generally as VEGF and/or VEGFr. The description below of the various aspects and embodiments of the invention is provided with reference to the exemplary VEGF and VEGFr (e.g., VEGFr1, VEGFr2,
 25 VEGFr3) genes referred to herein as VEGF and VEGFr respectively. However, the various aspects and embodiments are also directed to other VEGF and/or VEGFr genes, such as mutant VEGF and/or VEGFr genes, splice variants of VEGF and/or VEGFr genes, other VEGF and/or VEGFr ligands and receptors. The various aspects and embodiments are also directed to other genes that are involved in VEGF and/or VEGFr
 30 mediated pathways of signal transduction or gene expression that are involved in the progression, development, and/or maintenance of disease (e.g., cancer). These additional genes can be analyzed for target sites using the methods described for VEGF and/or VEGFr genes herein. Thus, the modulation of other genes and the effects of such

modulation of the other genes can be performed, determined, and measured as described herein.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a vascular endothelial growth factor (e.g., VEGF, VEGF-A, VEGF-B, VEGF-C, VEGF-D) gene, wherein said
5 siNA molecule comprises about 19 to about 21 base pairs.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a vascular endothelial growth factor receptor (e.g., VEGFr1, VEGFr2, and/or VEGFr3) gene, wherein said
10 siNA molecule comprises about 19 to about 21 base pairs.

In one embodiment, the invention features a siNA molecule that down-regulates expression of a VEGF gene, for example, wherein the VEGF gene comprises VEGF encoding sequence.

In one embodiment, the invention features a siNA molecule that down-regulates
15 expression of a VEGFr gene, for example, wherein the VEGFr gene comprises VEGFr encoding sequence.

In one embodiment, the invention features a siNA molecule having RNAi activity against VEGF and/or VEGFr RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having VEGF and/or VEGFr or other VEGF and/or VEGFr
20 encoding sequence, such as those sequences having GenBank Accession Nos. shown in **Table I**. In another embodiment, the invention features a siNA molecule having RNAi activity against VEGF and/or VEGFr RNA, wherein the siNA molecule comprises a sequence complementary to an RNA having other VEGF and/or VEGFr encoding sequence, for example mutant VEGF and/or VEGFr genes, splice variants of VEGF
25 and/or VEGFr genes, variants of VEGF and/or VEGFr genes with conservative substitutions, and homologous VEGF and/or VEGFr ligands and receptors. Chemical modifications as shown in **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the invention.

In one embodiment, the invention features a siNA molecule having RNAi activity
30 against VEGF and/or VEGFr RNA, wherein the siNA molecule comprises a sequence

complementary to any RNA having VEGF and/or VEGFr encoding sequence, such as those sequences having VEGF and/or VEGFr GenBank Accession Nos. shown in **Table I**. In another embodiment, the invention features a siNA molecule having RNAi activity against VEGF and/or VEGFr RNA, wherein the siNA molecule comprises a sequence
5 complementary to an RNA having other VEGF and/or VEGFr encoding sequence, for example, mutant VEGF and/or VEGFr genes, splice variants of VEGF and/or VEGFr genes, VEGF and/or VEGFr variants with conservative substitutions, and homologous VEGF and/or VEGFr ligands and receptors. Chemical modifications as shown in **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the
10 invention.

In another embodiment, the invention features a siNA molecule having RNAi activity against a VEGF and/or VEGFr gene, wherein the siNA molecule comprises nucleotide sequence complementary to nucleotide sequence of a VEGF and/or VEGFr gene, such as those VEGF and/or VEGFr sequences having GenBank Accession Nos.
15 shown in **Table I** or other VEGF and/or VEGFr encoding sequence, such as mutant VEGF and/or VEGFr genes, splice variants of VEGF and/or VEGFr genes, variants with conservative substitutions, and homologous VEGF and/or VEGFr ligands and receptors. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a VEGF and/or VEGFr gene and thereby
20 mediate silencing of VEGF and/or VEGFr gene expression, for example, wherein the siNA mediates regulation of VEGF and/or VEGFr gene expression by cellular processes that modulate the chromatin structure of the VEGF and/or VEGFr gene and prevent transcription of the VEGF and/or VEGFr gene.

In one embodiment, siNA molecules of the invention are used to down regulate or
25 inhibit the expression of soluble VEGF receptors (e.g. sVEGFr1 or sVEGFr2). Analysis of soluble VEGF receptor levels can be used to identify subjects with certain cancer types. These cancers can be amenable to treatment, for example, treatment with siNA molecules of the invention and any other chemotherapeutic composition. As such, analysis of soluble VEGF receptor levels can be used to determine treatment type and the
30 course of therapy in treating a subject. Monitoring of soluble VEGF receptor levels can be used to predict treatment outcome and to determine the efficacy of compounds and compositions that modulate the level and/or activity of VEGF receptors (see for example

Pavco USSN 10/438,493, incorporated by reference herein in its entirety including the drawings).

In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the
 5 siNA molecule that is complementary to a nucleotide sequence or portion of sequence of a VEGF and/or VEGFr gene. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence comprising a VEGF and/or VEGFr gene sequence or a portion thereof.

10 In one embodiment, the antisense region of VEGFr1 siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1-427, 1997-2000, 2009-2012, or 2244-2255. In one embodiment, the antisense region can also comprise sequence having any of SEQ ID NOs. 428-854, 2024-2027, 2032-2035, 2040-2043, 2188-2190, 2197-2200, 2203-2204, 2217, 2278-2280, 2292-2298, 2306-2318, 2326-
 15 2332, or 2340-2364. In another embodiment, the sense region of VEGFr1 constructs can comprise sequence having any of SEQ ID NOs. 1-427, 1997-2000, 2020-2023, 2028-2031, 2036-2039, 2185-2187, 2201-2202, 2218-2220, 2222, 2224, 2275-2277, 2281-2291, 2299-2305, 2319-2325, or 2333-2339. The sense region can comprise a sequence of SEQ ID NO. 2438 and the antisense region can comprise a sequence of SEQ ID NO.
 20 2439. The sense region can comprise a sequence of SEQ ID NO. 2440 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2442 and the antisense region can comprise a sequence of SEQ ID NO. 2443. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can
 25 comprise a sequence of SEQ ID NO. 2445 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2446.

In one embodiment, the antisense region of VEGFr2 siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 855-1178, 2001-
 30 2004, or 2017-2019 or 2256-2271. In one embodiment, the antisense region can also comprise sequence having any of SEQ ID NOs. 1179-1502, 2048-2051, 2056-2059,

2064-2067, 2208-2210, 2214-2216, 2226-2227, 2230-2231, 2377-2388, 2391-2392, 2401-2405, 2420-2423, 2448, 2450, 2452, or 2455. In another embodiment, the sense region of VEGFr2 constructs can comprise sequence having any of SEQ ID NOs. 855-1178, 2001-2004, 2017-2019, 2256-2271, 2044-2047, 2052-2055, 2060-2063, 2205-2207, 2211-2213, 2228-2229, 2365-2376, 2389-2390, 2393-2394, 2397-2400, 2406-2410, 2416-2419, 2424-2427, 2447, 2449, 2451, 2453, or 2454. The sense region can comprise a sequence of SEQ ID NO. 2438 and the antisense region can comprise a sequence of SEQ ID NO. 2439. The sense region can comprise a sequence of SEQ ID NO. 2440 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2442 and the antisense region can comprise a sequence of SEQ ID NO. 2443. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2445 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2446.

In one embodiment, the antisense region of VEGFr3 siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1503-1749, 2005-2008, or 2272-2274. In one embodiment, the antisense region can also comprise sequence having any of SEQ ID NOs. 1750-1996, 2072-2075, 2080-2083, 2088-2091, or 2435-2437. In another embodiment, the sense region of VEGFr3 constructs can comprise sequence having any of SEQ ID NOs. 1503-1749, 2005-2008, 2068-2071, 2076-2079, or 2084-2087, 2272-2274, or 2432-2434. The sense region can comprise a sequence of SEQ ID NO. 2438 and the antisense region can comprise a sequence of SEQ ID NO. 2439. The sense region can comprise a sequence of SEQ ID NO. 2440 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2442 and the antisense region can comprise a sequence of SEQ ID NO. 2443. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2445 and the antisense region can comprise a sequence of SEQ ID NO. 2441. The sense region can comprise a sequence of SEQ ID NO. 2444 and the antisense region can comprise a sequence of SEQ ID NO. 2446.

In one embodiment, a siNA molecule of the invention comprises any of SEQ ID NOs. 1-2455. The sequences shown in SEQ ID NOs: 1-2455 are not limiting. A siNA molecule of the invention can comprise any contiguous VEGF and/or VEGFr sequence (e.g., about 19 to about 25, or about 19, 20, 21, 22, 23, 24 or 25 contiguous VEGF and/or VEGFr nucleotides).

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank Accession Nos. shown in **Table I**. Chemical modifications in **Tables III and IV** and described herein can be applied to any siRNA construct of the invention.

In one embodiment of the invention a siNA molecule comprises an antisense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides, wherein the antisense strand is complementary to a RNA sequence encoding a VEGF and/or VEGFr protein, and wherein said siNA further comprises a sense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences with at least about 19 complementary nucleotides.

In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the antisense region is complementary to a RNA sequence encoding a VEGF and/or VEGFr protein, and wherein said siNA further comprises a sense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or more) nucleotides, wherein said sense region and said antisense region comprise a linear molecule with at least about 19 complementary nucleotides.

In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a VEGF and/or VEGFr protein. The siNA further comprises a sense strand, wherein said sense strand comprises a nucleotide sequence of a VEGF and/or VEGFr gene or a portion thereof.

In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence encoding a VEGF and/or VEGFr protein or a portion thereof. The siNA molecule further comprises a sense region, wherein said sense region comprises a nucleotide
5 sequence of a VEGF and/or VEGFr gene or a portion thereof.

In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a VEGFr gene. Because VEGFr genes can share some degree of sequence homology with each other, siNA molecules can be designed to target a class of VEGFr genes (and associated receptor or ligand genes) or
10 alternately specific VEGFr genes by selecting sequences that are either shared amongst different VEGFr targets or alternatively that are unique for a specific VEGFr target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of VEGFr RNA sequence having homology between several VEGFr genes so as to target several VEGFr genes (e.g., VEGFr1, VEGFr2 and/or VEGFr3, different VEGFr
15 isoforms, splice variants, mutant genes etc.) with one siNA molecule. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific VEGFr RNA sequence due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

In one embodiment, a siNA molecule of the invention has RNAi activity that
20 modulates expression of RNA encoded by a VEGF gene. Because VEGF genes can share some degree of sequence homology with each other, siNA molecules can be designed to target a class of VEGF genes (and associated receptor or ligand genes) or alternately specific VEGF genes by selecting sequences that are either shared amongst different VEGF targets or alternatively that are unique for a specific VEGF target.
25 Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of VEGF RNA sequence having homology between several VEGF genes so as to target several VEGF genes (e.g., VEGF-A, VEGF-B, VEGF-C and/or VEGF-D, different VEGF isoforms, splice variants, mutant genes etc.) with one siNA molecule. In another embodiment, the siNA molecule can be designed to target a sequence that is
30 unique to a specific VEGF RNA sequence due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid molecules. In another embodiment, the siNA molecules of the invention consist of duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24 or 25) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplexes with overhanging ends of about about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotides, for example, about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs.

In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for VEGF and/or VEGFr expressing nucleic acid molecules, such as RNA encoding a VEGF and/or VEGFr protein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical modifications, when used in various siNA constructs, are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al.*, *supra*, applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA constructs.

In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (*e.g.*, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA. If the siNA

molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

One aspect of the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene. In one embodiment, a double stranded siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 21 nucleotides long.

10 In one embodiment, the double-stranded siNA molecule does not contain any ribonucleotides. In another embodiment, the double-stranded siNA molecule comprises one or more ribonucleotides. In one embodiment, each strand of the double-stranded siNA molecule comprises about 19 to about 23 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides, wherein each strand comprises about 19 nucleotides that are

15 complementary to the nucleotides of the other strand. In one embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof of the VEGF and/or VEGFr gene, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence of the VEGF and/or

20 VEGFr gene or a portion thereof.

In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene comprising an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of the VEGF and/or

25 VEGFr gene or a portion thereof, and a sense region, wherein the sense region comprises a nucleotide sequence substantially similar to the nucleotide sequence of the VEGF and/or VEGFr gene or a portion thereof. In one embodiment, the antisense region and the sense region each comprise about 19 to about 23 (e.g. about 19, 20, 21, 22, or 23) nucleotides, wherein the antisense region comprises about 19 nucleotides that are

30 complementary to nucleotides of the sense region.

In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the VEGF and/or VEGFr gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. The sense region can be connected to the antisense region via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the VEGF and/or VEGFr gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the siNA molecule has one or more modified pyrimidine and/or purine nucleotides. In one embodiment, the pyrimidine nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides or 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In one embodiment, the pyrimidine nucleotides in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the antisense region are 2'-O-methyl or 2'-deoxy purine nucleotides. In another embodiment of any of the above-described siNA

molecules, any nucleotides present in a non-complementary region of the sense strand (e.g. overhang region) are 2'-deoxy nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein the fragment comprising the sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the fragment. In another embodiment, the terminal cap moiety is an inverted deoxy abasic moiety or glyceryl moiety. In another embodiment, each of the two fragments of the siNA molecule comprise about 21 nucleotides.

In one embodiment, the invention features a siNA molecule comprising at least one modified nucleotide, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. The siNA can be, for example, of length between about 12 and about 36 nucleotides. In another embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In another embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In another embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as phosphorothioate linkage. In another embodiment, the 2'-deoxy-2'-fluoronucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides. In another embodiment, the siNA comprises a sequence that is complementary to a nucleotide sequence in a separate RNA, such as a VEGF or VEGFr RNA.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the VEGF and/or VEGFr gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the purine nucleotides present in the antisense region comprise 2'-deoxy- purine nucleotides. In an alternative embodiment, the purine nucleotides present in the antisense region comprise 2'-O-methyl purine nucleotides. In either of the above embodiments, the antisense region can comprise a phosphorothioate internucleotide linkage at the 3' end of the antisense region. Alternatively, in either of the above embodiments, the antisense region can comprise a glyceryl modification at the 3' end of the antisense region. In another embodiment of any of the above-described siNA molecules, any nucleotides present in a non-complementary region of the antisense strand (e.g. overhang region) are 2'-deoxy nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a VEGF and/or VEGFr gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In another embodiment about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule and wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine nucleotide, such as a 2'-deoxy-thymidine. In another embodiment, all 21 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the VEGF and/or VEGFr gene. In another embodiment, about 21 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the VEGF and/or

VEGFr gene. In any of the above embodiments, the 5'-end of the fragment comprising said antisense region can optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of a VEGF and/or VEGFr RNA sequence (e.g., wherein said target RNA sequence is encoded by a VEGF and/or VEGFr gene involved in the VEGF and/or VEGFr pathway), wherein the siNA molecule does not contain any ribonucleotides and wherein each strand of the double-stranded siNA molecule is about 21 nucleotides long. Examples of non-ribonucleotide containing siNA constructs are combinations of stabilization chemistries shown in Table IV in any combination of Sense/Antisense chemistries, such as Stab 7/8, Stab 7/11, Stab 8/8, Stab 18/8, Stab 18/11, Stab 12/13, Stab 7/13, or Stab 18/13.

In one embodiment, the invention features a medicament comprising a siNA molecule of the invention.

In one embodiment, the invention features an active ingredient comprising a siNA molecule of the invention.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule to down-regulate expression of a VEGF and/or VEGFr gene, wherein the siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 21 nucleotides long.

In one embodiment, a VEGFr gene contemplated by the invention is a VEGFr1, VEGFr2, or VEGFr3 gene.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, the VEGFr gene is VEGFr2. In one embodiment, the VEGFr gene is VEGFr1.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA that encodes a protein or portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, each strand of the siNA molecule comprises about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides, wherein each strand comprises at least about 19 nucleotides that are complementary to the nucleotides of the other strand. In another embodiment, the siNA molecule is assembled from two oligonucleotide fragments, wherein one fragment comprises the nucleotide sequence of the antisense strand of the siNA molecule and a second fragment comprises nucleotide sequence of the sense region of the siNA molecule. In yet another embodiment, the sense strand is connected to the

antisense strand via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker. In a further embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In still another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-deoxy purine nucleotides. In another embodiment, the antisense strand comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides and one or more 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-O-methyl purine nucleotides. In a further embodiment the sense strand comprises a 3'-end and a 5'-end, wherein a terminal cap moiety (e.g., an inverted deoxy abasic moiety or inverted deoxy nucleotide moiety such as inverted thymidine) is present at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the sense strand. In another embodiment, the antisense strand comprises a phosphorothioate internucleotide linkage at the 3' end of the antisense strand. In another embodiment, the antisense strand comprises a glyceryl modification at the 3' end. In another embodiment, the 5'-end of the antisense strand optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein each of the two strands of the siNA molecule comprises about 21 nucleotides. In one embodiment, about 21 nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule. In another embodiment, about 19 nucleotides of each strand of the siNA molecule are base-

paired to the complementary nucleotides of the other strand of the siNA molecule, wherein at least two 3' terminal nucleotides of each strand of the siNA molecule are not base-paired to the nucleotides of the other strand of the siNA molecule. In another embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine, such as 2'-deoxy-thymidine. In another embodiment, each strand of the siNA molecule is base-paired to the complementary nucleotides of the other strand of the siNA molecule. In another embodiment, about 19 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the VEGF and/or VEGFr RNA or a portion thereof. In another embodiment, about 21 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the VEGF and/or VEGFr RNA or a portion thereof.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the 5'-end of the antisense strand optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the nucleotide sequence or a portion thereof of the antisense strand is complementary to a nucleotide sequence of the untranslated region or a portion thereof of the VEGF and/or VEGFr RNA.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a VEGF and/or VEGFr gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of VEGF and/or VEGFr RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the nucleotide sequence of the antisense strand is complementary to a nucleotide sequence of the VEGF and/or VEGFr RNA or a portion thereof that is present in the VEGF and/or VEGFr RNA.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention in a pharmaceutically acceptable carrier or diluent.

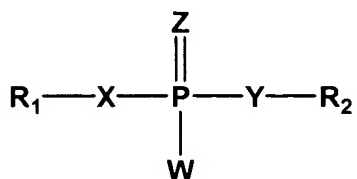
In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity in humans.

In any of the embodiments of siNA molecules described herein, the antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. In any of the embodiments

of siNA molecules described herein, the antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding VEGF and/or VEGFr and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:

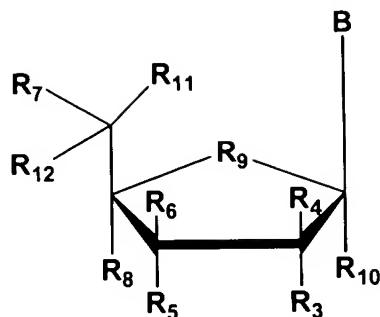


wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y

is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or acetyl and wherein W, X, Y, and Z are optionally not all O. In another embodiment, a backbone modification of the invention comprises a phosphonoacetate and/or thiophosphonoacetate internucleotide
5 linkage (see for example Sheehan et al., 2003, Nucleic Acids Research, 31, 4109-4118).

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can
10 comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having
15 Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example,
20 an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide
25 or non-nucleotide having any of Formulae I-VII.

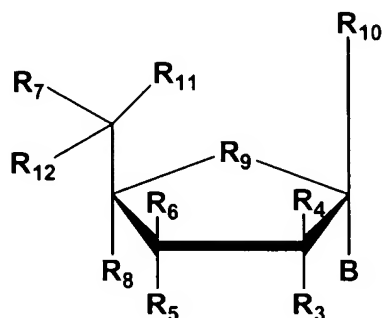
In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more)
30 nucleotides or non-nucleotides having Formula II:



wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:



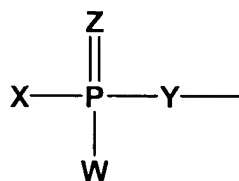
wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-

modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of
 5 Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-
 10 end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



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wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, alkylhalo, or acetyl; and wherein W, X, Y and Z are not all O.

In one embodiment, the invention features a siNA molecule having a 5'-terminal
 20 phosphate group having Formula IV on the target-complementary strand, for example, a strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or
 25 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-

complementary strand of a siNA molecule of the invention, for example a siNA molecule having chemical modifications having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends

of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more

phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate

internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5, specifically about 1, 2, 3, 4, 5 or
5 more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the 2'-5' internucleotide linkage(s) can be present at various other positions within one or
10 both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

15 In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification
20 comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and
25 wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of
30 Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having

about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 25 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 3 to about 23 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, a linear hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

In another embodiment, a siNA molecule of the invention comprises an asymmetric hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 20 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10,

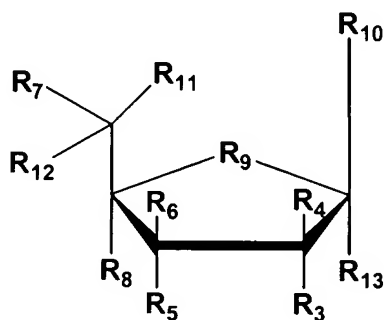
11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35
 5 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms an asymmetric hairpin structure having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18) base pairs and a 5'-terminal phosphate group that can be chemically
 10 modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, an asymmetric hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, an asymmetric hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

15 In another embodiment, a siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 16 to about 25 (e.g., about 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides in length, wherein the sense region is about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,
 20 or 18) nucleotides in length, wherein the sense region and the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises an asymmetric double stranded structure having separate
 25 polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 18 to about 22 (e.g., about 18, 19, 20, 21, or 22) nucleotides in length and wherein the sense region is about 3 to about 15 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15) nucleotides in length, wherein the sense region the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more
 30 chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. In another embodiment, the asymmetric double stranded siNA molecule can also have a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV).

In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

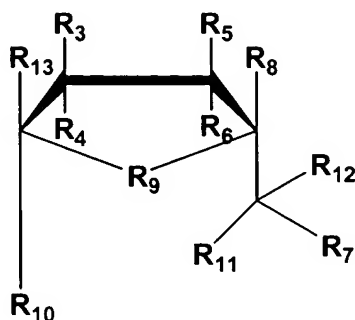
In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid,

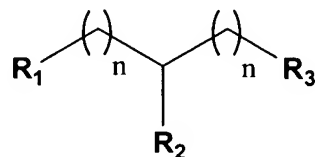
O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R₉ is O, S, CH₂, S=O, CHF, or CF₂.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a
5 compound having Formula VI:



wherein each R₃, R₄, R₅, R₆, R₇, R₈, R₁₀, R₁₁, R₁₂, and R₁₃ is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-
10 alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R₉ is O, S, CH₂, S=O, CHF, or CF₂, and either R₂, R₃, R₈ or R₁₃ serve as points of attachment to the siNA molecule of the
15 invention.

In another embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



20 wherein each *n* is independently an integer from 1 to 12, each R₁, R₂ and R₃ is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl,

alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having Formula I, and
 5 R₁, R₂ or R₃ serves as points of attachment to the siNA molecule of the invention.

In another embodiment, the invention features a compound having Formula VII, wherein R₁ and R₂ are hydroxyl (OH) groups, n = 1, and R₃ comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA
 10 molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in **Figure 10**).

In another embodiment, a moiety having any of Formula V, VI or VII of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of the invention. For example, a moiety having Formula V, VI or VII can be present at the
 15 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the
 20 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for
 25 example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA
 30 molecule.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

10 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

30 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any

(*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

10 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

20 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

30 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein

any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or
 5 more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein
 10 any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine
 15 nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFr inside a cell or reconstituted *in vitro* system
 20 comprising a sense region, wherein one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*,
 25 wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and an antisense region, wherein one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-
 30 2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-

O-methyl purine nucleotides). The sense region and/or the antisense region can have a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense and/or antisense sequence. The sense and/or antisense region can optionally further comprise a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides. The overhang nucleotides can further comprise one or more (e.g., about 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Tables III and IV** herein.

In any of these described embodiments, the purine nucleotides present in the sense region are alternatively 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides) and one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Also, in any of these embodiments, one or more purine nucleotides present in the sense region are alternatively purine ribonucleotides (e.g., wherein all purine nucleotides are purine ribonucleotides or alternately a plurality of purine nucleotides are purine ribonucleotides) and any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Additionally, in any of these embodiments, one or more purine nucleotides present in the sense region and/or present in the antisense region are alternatively selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides).

In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention,

but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides.

In one embodiment, the sense strand of a double stranded siNA molecule of the invention comprises a terminal cap moiety, (see for example **Figure 10**) such as an inverted deoxyabasic moiety, at the 3'-end, 5'-end, or both 3' and 5'-ends of the sense strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) against a VEGF and/or VEGFR inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule. Non-limiting examples of conjugates contemplated by the invention include conjugates and ligands described in Vargeese *et al.*, USSN 10/427,160, filed April 30, 2003, incorporated by reference herein in its entirety, including the drawings. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the

antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate molecule
5 attached to the chemically-modified siNA molecule is a poly ethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.*, U.S. Serial No. 10/201,394, incorporated by reference herein. The type of conjugates
10 used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses
15 improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the
20 siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of ≥ 2 nucleotides in length, for example about 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic
25 acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of
30 the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.*, 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin.*

Mol. Ther., 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma *et al.*, *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand *et al.*, *Nucleic Acids Res.* 1990, 18:6353; McCurdy *et al.*, *Nucleosides & Nucleotides* 1991, 10:287; Jsche *et al.*, *Tetrahedron Lett.* 1993, 34:301; Ono *et al.*, *Biochemistry* 1991, 30:9914; Arnold *et al.*, International Publication No. WO 89/02439; Usman *et al.*, International Publication No. WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. For example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA comprise separate oligonucleotides not having any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotides. In another example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA are linked or circularized by a nucleotide or non-nucleotide linker as described herein, wherein the oligonucleotide does not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotide.

Applicant has surprisingly found that the presense of ribonucleotides (e.g., nucleotides having a 2'-hydroxyl group) within the siNA molecule is not required or essential to support RNAi activity. As such, in one embodiment, all positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and
5 or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system
10 comprising a single stranded polynucleotide having complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the
15 single stranded siNA molecule of the invention comprises about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides
20 such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system comprising
25 a single stranded polynucleotide having complementarity to a target nucleic acid sequence, wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present
30 in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as

any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The siNA optionally further comprises about 1 to about 4 or more (e.g., about 1, 2, 3, 4 or more) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal

5 nucleotides can further comprise one or more (e.g., 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group. In any of these embodiments, any purine nucleotides present in the antisense region are alternatively 2'-deoxy purine nucleotides (e.g., wherein all purine

10 nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA (i.e., purine nucleotides present in the sense and/or antisense region) can alternatively be locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine

15 nucleotides are LNA nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA are alternatively 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides). In another embodiment, any modified nucleotides present in the single stranded siNA

20 molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present

25 in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

In one embodiment, the invention features a method for modulating the expression of a VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA

30 strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the cell.

In one embodiment, the invention features a method for modulating the expression of a VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the cell.

In another embodiment, the invention features a method for modulating the expression of two or more VEGF and/or VEGFr genes within a cell comprising: (a) synthesizing one or more siNA molecules of the invention, which can be chemically-modified, wherein the siNA strands comprise sequences complementary to RNA of the VEGF and/or VEGFr genes and wherein the sense strand sequences of the siNAs comprise sequences identical or substantially similar to the sequences of the target RNAs; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequences of the target RNAs; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the cell.

In one embodiment, siNA molecules of the invention are used as reagents in ex vivo applications. For example, siNA reagents are introduced into tissue or cells that are transplanted into a subject for therapeutic effect. The cells and/or tissue can be derived from an organism or subject that later receives the explant, or can be derived from another organism or subject prior to transplantation. The siNA molecules can be used to modulate the expression of one or more genes in the cells or tissue, such that the cells or tissue obtain a desired phenotype or are able to perform a function when transplanted in vivo. In one embodiment, certain target cells from a patient are extracted. These extracted cells are contacted with siNAs targeting a specific nucleotide sequence within the cells under conditions suitable for uptake of the siNAs by these cells (e.g. using delivery reagents such as cationic lipids, liposomes and the like or using techniques such as electroporation to facilitate the delivery of siNAs into cells). The cells are then reintroduced back into the same patient or other patients. In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in that organism.

In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another

organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one VEGF and/or VEGFr gene in a tissue explant comprising:

5 (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr genes; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the tissue explant. In another

10 embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in an organism comprising: (a) synthesizing a siNA

15 molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the organism. The level of VEGF or VEGFr can be determined as is known in the art or as described in Pavco

20 USSN 10/438,493, incorporated by reference herein in its entirety including the drawings.

In another embodiment, the invention features a method of modulating the expression of more than one VEGF and/or VEGFr gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified,

25 wherein one of the siNA strands comprises a sequence complementary to RNA of the VEGF and/or VEGFr genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the organism. The level of VEGF or VEGFr can be determined as is known in the art or as described in Pavco USSN 10/438,493, incorporated by reference herein in its

30 entirety including the drawings.

In one embodiment, the invention features a method for modulating the expression of a VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one VEGF and/or VEGFr gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) contacting the cell in vitro or in vivo with the siNA molecule under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) contacting the cell of the tissue explant derived from a particular organism with the siNA molecule under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one VEGF and/or VEGFr gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back

into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one VEGF and/or VEGFr gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the VEGF and/or VEGFr gene; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a VEGF and/or VEGFr gene in an organism comprising contacting the organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the VEGF and/or VEGFr gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one VEGF and/or VEGFr gene in an organism comprising contacting the organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the VEGF and/or VEGFr genes in the organism.

The siNA molecules of the invention can be designed to down regulate or inhibit target (VEGF and/or VEGFr) gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s),

post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families such as VEGF and/or VEGFr family genes. As such, siNA molecules targeting multiple VEGF and/or VEGFr targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, the progression and/or maintenance of cancer.

In one embodiment, siNA molecule(s) and/or methods of the invention are used to down regulate the expression of gene(s) that encode RNA referred to by Genbank Accession, for example VEGF and/or VEGFr genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example, Genbank Accession Nos. shown in **Table I**.

In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In one embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4^N , where N represents the number of base paired nucleotides in each of the siNA construct strands (*eg.* for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be 4^{19}); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target VEGF and/or VEGFr RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 7 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of VEGF and/or VEGFr RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target VEGF and/or VEGFr RNA sequence. The target VEGF and/or VEGFr RNA sequence can be obtained as is known in the art,

for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable

carrier or diluent. In another embodiment, the invention features a method for diagnosing a disease or condition in a subject comprising administering to the subject a composition of the invention under conditions suitable for the diagnosis of the disease or condition in the subject. In another embodiment, the invention features a method for
5 treating or preventing a disease or condition in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other therapeutic compounds. In yet another embodiment, the invention features a method for reducing or preventing tissue rejection in a subject comprising administering
10 to the subject a composition of the invention under conditions suitable for the reduction or prevention of tissue rejection in the subject.

In another embodiment, the invention features a method for validating a VEGF and/or VEGFr gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes
15 a sequence complementary to RNA of a VEGF and/or VEGFr target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the VEGF and/or VEGFr target gene in the cell, tissue, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

20 In another embodiment, the invention features a method for validating a VEGF and/or VEGFr target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a VEGF and/or VEGFr target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of
25 the VEGF and/or VEGFr target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

By “biological system” is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human, animal, plant, insect, bacterial, viral or other sources, wherein the system comprises the components required for RNAi
30 acitivity. The term “biological system” includes, for example, a cell, tissue, or organism,

or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a VEGF and/or VEGFr target gene in a biological system, including, for example, in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one VEGF and/or VEGFr target gene in a biological system, including, for example, in a cell, tissue, or organism.

In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts as a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety that can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide

sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

5 In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

10 In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of Formulae I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

15 In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

20 In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

25 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the

antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

5 In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

10 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence.

15 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for
20 isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulate the polymerase activity of a
25 cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology
30 to a chemically-modified siNA molecule comprising (a) introducing nucleotides having

any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the
5 chemically-modified siNA molecule.

In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against a VEGF and/or VEGFr in a cell, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a
10 manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against VEGF and/or VEGFr comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable
15 for isolating siNA molecules having improved RNAi activity.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a VEGF and/or VEGFr target RNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under
20 conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a VEGF and/or VEGFr target DNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination
25 thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target DNA.

In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more

chemical modifications described herein that modulates the cellular uptake of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules against VEGF and/or VEGFr with improved cellular uptake comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

In one embodiment, the invention features siNA constructs that mediate RNAi against a VEGF and/or VEGFr, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such conjugates are described in Vargeese *et al.*, U.S. Serial No. 10/201,394 incorporated by reference herein.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability, comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; cholesterol; polyamines, such as spermine or spermidine; and others.

The term “ligand” refers to any compound or molecule, such as a drug, peptide, hormone, or neurotransmitter, that is capable of interacting with another compound, such as a receptor, either directly or indirectly. The receptor that interacts with a ligand can be present on the surface of a cell or can alternately be an intercellular receptor. Interaction of the ligand with the receptor can result in a biochemical reaction, or can simply be a physical interaction or association.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

5 Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, nanoparticles, receptors, ligands, and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

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In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 2,000 to about 50,000 daltons (Da).

15 The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include a siNA molecule of the invention and a vehicle that promotes introduction of the siNA into cells of interest as described herein (e.g., using lipids and other methods of transfection

20 known in the art, see for example Beigelman *et al.*, US 6,395,713). The kit can be used for target validation, such as in determining gene function and/or activity, or in drug optimization, and in drug discovery (see for example Usman *et al.*, USSN 60/402,996). Such a kit can also include instructions to allow a user of the kit to practice the invention.

The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication, for example by mediating RNA interference "RNAi" or gene silencing in a sequence-specific manner; see for example Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.*, 2001, *Nature*, 411, 494-498; and Kreutzer *et al.*, International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.*, International PCT

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Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.*, International PCT Publication No. WO 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.*, International PCT Publication No. WO 00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002, *Science*, 297, 2056-60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non limiting examples of siNA molecules of the invention are shown in **Figures 4-6**, and **Tables II, III, and IV** herein. For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 19 base pairs); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense

regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo* or *in vitro* to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell.*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiment, the siNA molecule of the invention comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linker molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der Waals interactions, hydrophobic interactions, and/or stacking interactions. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30,

40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237).

By "asymmetric hairpin" as used herein is meant a linear siNA molecule comprising an antisense region, a loop portion that can comprise nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g., about 19, 20, 21, or 22) nucleotides) and a loop region comprising about 4 to about 8 (e.g., about 4, 5, 6, 7, or 8) nucleotides, and a sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region. The asymmetric hairpin siNA molecule can also comprise a 5'-terminal phosphate group that can be chemically modified. The loop portion of the asymmetric hairpin siNA molecule can comprise nucleotides, non-nucleotides, linker molecules, or conjugate molecules as described herein.

By "asymmetric duplex" as used herein is meant a siNA molecule having two separate strands comprising a sense region and an antisense region, wherein the sense region comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and
 5 form a duplex. For example, an asymmetric duplex siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g. about 19, 20, 21, or 22) nucleotides) and a sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region.

10 By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the
 15 use of the word "modulate" is not limited to this definition.

By "inhibit", "down-regulate", or "reduce", it is meant that the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, is reduced below that observed in the absence of the nucleic acid molecules (e.g., siNA) of
 20 the invention. In one embodiment, inhibition, down-regulation or reduction with an siNA molecule is below that level observed in the presence of an inactive or attenuated molecule. In another embodiment, inhibition, down-regulation, or reduction with siNA molecules is below that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment,
 25 inhibition, down-regulation, or reduction of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence.

By "gene" or "target gene" is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding
 30 a polypeptide. The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is

present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates.

5 Non-limiting examples of fungi include molds or yeasts.

By “VEGF” as used herein is meant, any vascular endothelial growth factor (e.g., VEGF, VEGF-A, VEGF-B, VEGF-C, VEGF-D) protein, peptide, or polypeptide having vascular endothelial growth factor activity, such as encoded by VEGF Genbank Accession Nos. shown in **Table I**. The term VEGF also refers to nucleic acid sequences
10 encoding any vascular endothelial growth factor protein, peptide, or polypeptide having vascular endothelial growth factor activity.

By “VEGF-B” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_003377, having vascular endothelial growth factor type B activity. The term VEGF-B also refers to nucleic acid
15 sequences encoding any VEGF-B protein, peptide, or polypeptide having VEGF-B activity.

By “VEGF-C” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_005429, having vascular endothelial growth factor type C activity. The term VEGF-C also refers to nucleic acid
20 sequences encoding any VEGF-C protein, peptide, or polypeptide having VEGF-C activity.

By “VEGF-D” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_004469, having vascular endothelial growth factor type D activity. The term VEGF-D also refers to nucleic acid
25 sequences encoding any VEGF-D protein, peptide, or polypeptide having VEGF-D activity.

By “VEGFr” as used herein is meant, any vascular endothelial growth factor receptor protein, peptide, or polypeptide (e.g., VEGFr1, VEGFr2, or VEGFr3, including both membrane bound and/or soluble forms thereof) having vascular endothelial growth
30 factor receptor activity, such as encoded by VEGFr Genbank Accession Nos. shown in

Table I. The term VEGFr also refers to nucleic acid sequences encoding any vascular endothelial growth factor receptor protein, peptide, or polypeptide having vascular endothelial growth factor receptor activity.

By “VEGFr1” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_002019, having vascular endothelial growth factor receptor type 1 (*flt*) activity, for example, having the ability to bind a vascular endothelial growth factor. The term VEGF1 also refers to nucleic acid sequences encoding any VEGFr1 protein, peptide, or polypeptide having VEGFr1 activity.

By “VEGFr2” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_002253, having vascular endothelial growth factor receptor type 2 (*kdr*) activity, for example, having the ability to bind a vascular endothelial growth factor. The term VEGF2 also refers to nucleic acid sequences encoding any VEGFr2 protein, peptide, or polypeptide having VEGFr2 activity.

By “VEGFr3” is meant, protein, peptide, or polypeptide receptor or a derivative thereof, such as encoded by Genbank Accession No. NM_002020 having vascular endothelial growth factor receptor type 3 (*kdr*) activity, for example, having the ability to bind a vascular endothelial growth factor. The term VEGF3 also refers to nucleic acid sequences encoding any VEGFr3 protein, peptide, or polypeptide having VEGFr3 activity.

By “highly conserved sequence region” is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

By “sense region” is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By “antisense region” is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a

siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

By "target nucleic acid" is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

5 By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity.

10 Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.*, 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*, 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick

15 base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, or 10 nucleotides out of a total of 10 nucleotides in the first oligonucleotide being base paired to a second nucleic acid sequence having 10 nucleotides represents 50%, 60%, 70%, 80%, 90%, and 100% complementary respectively). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same

20 number of contiguous residues in a second nucleic acid sequence.

The siRNA molecules of the invention represent a novel therapeutic approach to treat a variety of pathologic indications or other conditions, such as tumor angiogenesis and cancer, including but not limited to breast cancer, lung cancer (including non-small cell lung carcinoma), prostate cancer, colorectal cancer, brain cancer, esophageal cancer,

25 bladder cancer, pancreatic cancer, cervical cancer, head and neck cancer, skin cancers, nasopharyngeal carcinoma, liposarcoma, epithelial carcinoma, renal cell carcinoma, gallbladder adenocarcinoma, parotid adenocarcinoma, ovarian cancer, melanoma, lymphoma, glioma, endometrial sarcoma, multidrug resistant cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration,

30 arthritis, psoriasis, endometriosis, female reproduction, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber

syndrome, Osler-Weber-Rendu syndrome, renal disease such as Autosomal dominant polycystic kidney disease (ADPKD), and any other diseases or conditions that are related to or will respond to the levels of VEGF, VEGFr1, VEGFr2 and/or VEGFr3 in a cell or tissue, alone or in combination with other therapies. The reduction of VEGF, VEGFr1, VEGFr2 and/or VEGFr3 expression (specifically VEGF, VEGFr1, VEGFr2 and/or VEGFr3 gene RNA levels) and thus reduction in the level of the respective protein relieves, to some extent, the symptoms of the disease or condition.

In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to about 23 base pairs (*e.g.*, about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (*e.g.*, about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (*e.g.*, 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (*e.g.*, about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Table II**. Exemplary synthetic siNA molecules of the invention are shown in **Tables III and IV** and/or **Figures 4-5**.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, *e.g.*, specifically does not refer to a human. The cell can be present in an organism, *e.g.*, birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (*e.g.*, bacterial cell) or eukaryotic (*e.g.*, mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables II-III** and/or **Figures 4-**

5. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells.

The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

The term "phosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise an acetyl or protected acetyl group.

The term "thiophosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z comprises an acetyl or protected acetyl group and

W comprises a sulfur atom or alternately W comprises an acetyl or protected acetyl group and Z comprises a sulfur atom.

5 The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

10 The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein (e.g., cancers and other proliferative conditions). For example, to treat a particular
15 disease or condition, the siNA molecules can be administered to a subject or can be administered to other appropriate cells evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the
20 described molecules could be used in combination with one or more known therapeutic agents to treat a disease or condition. Non-limiting examples of other therapeutic agents that can be readily combined with a siNA molecule of the invention are enzymatic nucleic acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and
25 other organic and/or inorganic compounds including metals, salts and ions.

In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector
30 can also contain sequence(s) encoding a single nucleic acid molecule that is self-

complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

Figure 2 shows a MALDI-TOF mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

Figure 3 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

Figure 4A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N). Various
 5 modifications are shown for the sense and antisense strands of the siNA constructs.

Figure 4A: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.
 10 The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide
 15 linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s" connects the (N N) nucleotides in the antisense strand.

Figure 4B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may
 20 be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-
 25 nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified
 30 internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s" connects the (N N) nucleotides in the sense and antisense strand.

Figure 4C: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s" connects the (N N) nucleotides in the antisense strand.

Figure 4D: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s" connects the (N N) nucleotides in the antisense strand.

Figure 4E: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides,

deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand.

Figure 4F: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of the invention. Furthermore, when a glyceryl moiety (L) is present at the 3'-end of the antisense strand for any construct shown in Figure 4 A-F, the modified internucleotide linkage is optional.

Figure 5A-F shows non-limiting examples of specific chemically-modified siNA sequences of the invention. **A-F** applies the chemical modifications described in **Figure**

4A-F to a VEGFr2 siNA sequence. Such chemical modifications can be applied to any sequence herein, such as any VEGF, VEGFr1, VEGFr2, or VEGFr3 sequence.

Figure 6 shows non-limiting examples of different siNA constructs of the invention. The examples shown (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 *in vivo* and/or *in vitro*. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 *in vivo* and/or *in vitro*, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 *in vivo* and/or *in vitro*. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use *in vivo* or *in vitro* and/or *in vitro*.

Figure 7A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate siNA hairpin constructs.

Figure 7A: A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined VEGF and/or VEGFr target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

Figure 7B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a VEGF and/or VEGFr target sequence and having self-complementary sense and antisense regions.

Figure 7C: The construct is heated (for example to about 95°C) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed
 5 such that a 3'-terminal nucleotide overhang results from the transcription, for example by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul *et al.*, 2002, *Nature Biotechnology*, 29, 505-508.

Figure 8A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

10 **Figure 8A:** A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined VEGF and/or VEGFr target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined
 15 sequence (X).

Figure 8B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

Figure 8C: The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector
 20 for expression in cells. The transcription cassette is designed such that a U6 promoter region flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

Figure 9A-E is a diagrammatic representation of a method used to determine
 25 target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as messenger RNA.

Figure 9A: A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary
 30 to the antisense region of the siNA.

Figure 9B&C: (Figure 9B) The sequences are pooled and are inserted into vectors such that (Figure 9C) transfection of a vector into cells results in the expression of the siNA.

Figure 9D: Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

Figure 9E: The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

Figure 10 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3'-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

Figure 11 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-mofications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

Figure 12 shows a non-limiting example of siNA mediated inhibition of VEGF-induced angiogenesis using the rat corneal model of angiogenesis. siNA targeting site 2340 of VEGFr1 RNA (shown as RPI No. 29695/29699 sense strand/antisense strand) was compared to an inverted control siNA (shown as RPI No. 29983/29984 sense strand/antisense strand) at three different concentrations (1ug, 3ug, and 10ug) and compared to a VEGF control in which no siNA was administered. As shown in the Figure, siNA constructs targeting VEGFr1 RNA can provide significant inhibition of angiogenesis in the rat corneal model.

Figure 13 shows a non-limiting example of reduction of VEGFr1 mRNA in A375 cells mediated by chemically-modified siNAs that target VEGFr1 mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs (Stabilization “Stab” chemistries are shown in **Table IV**, constructs are referred to by RPI number, see **Table III**) comprising Stab 4/5 chemistry (RPI 31190/31193), Stab 1/2 chemistry (RPI 31183/31186 and RPI 31184/31187), and unmodified RNA (RPI 30075/30076) were compared to untreated cells, matched chemistry inverted control siNA constructs, (RPI 31208/31211, RPI 31201/31204, RPI 31202/31205, and RPI 30077/30078) scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). All of the siNA constructs show significant reduction of VEGFr1 RNA expression.

Figure 14 shows non-limiting examples of phosphorylated siNA molecules of the invention, including linear and duplex constructs and asymmetric derivatives thereof.

Figure 15 shows non-limiting examples of chemically modified terminal phosphate groups of the invention.

Figure 16 shows a non-limiting example of inhibition of VEGF induced neovascularization in the rat corneal model. VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273) was tested for inhibition of VEGF-induced angiogenesis at three different concentrations (2.0 ug, 1.0 ug, and 0.1 ug dose response) as compared to a matched chemistry inverted control siNA construct (Compound No. 31276/31279) at each concentration and a VEGF control in which no siNA was administered. As shown in the figure, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is highly effective in inhibiting VEGF-

induced angiogenesis in the rat corneal model compared to the matched chemistry inverted control siNA at concentrations from 0.1 ug to 2.0 ug.

Figure 17 shows a non-limiting example of inhibition of VEGF induced neovascularization in a mouse model of coroidal neovascularization via intraocular administration of siNA. VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273) was tested for inhibition of neovascularization at two different concentrations (1.5 ug, and 0.5 ug) as compared to a matched chemistry inverted control siNA construct (Compound No. 31276/31279) and phosphate buffered saline (PBS). siNA constructs were administered intraocularly on days 1 and 7 following laser induced injury to the choroid, and choroidal neovascularization assessed on day 14. As shown in the figure, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is highly effective in inhibiting neovascularization via intraocular administration in this model.

Figure 18 shows a non-limiting example of inhibition of VEGF induced neovascularization in a mouse model of coroidal neovascularization via periocular administration of siNA. VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273) was tested for inhibition of neovascularization at two different concentrations (1.5 ug with a saline control, and 0.5 ug with an inverted siNA control, Compound No. 31276/31279). Eight mice were used in each arm of the study with one eye receiving the active siNA and the other eye receiving the saline or inverted control. siNA constructs and controls were administered daily up to 14 days, and neovascularization was assessed at day 17 following laser induced injury to the choroid. As shown in the figure, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is highly effective in inhibiting neovascularization via periocular administration in this model.

Figure 19 shows another non-limiting example of inhibition of VEGF induced neovascularization in a mouse model of coroidal neovascularization via periocular administration of siNA. VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273) was tested for inhibition of neovascularization at two different concentrations (1.5 ug with an inverted siNA control, Compound No. 31276/31279 and 0.5 ug with a saline control). Nine mice were used in the active

versus inverted arm of the study with one eye receiving the active siNA and the other eye receiving the inverted control. Eight mice were used in the active versus saline arm of the study with one eye receiving the active siNA and the other eye receiving the saline control. siNA constructs and controls were administered daily up to 14 days, and
 5 neovascularization was assessed at day 17 following laser induced injury to the choroid. As shown in the figure, the active siNA construct having "Stab 9/10" chemistry (Compound No. 31270/31273) is highly effective in inhibiting neovascularization via periocular administration in this model.

DETAILED DESCRIPTION OF THE INVENTION

10 Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity
 15 to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or "improved RNAi activity" is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate
 20 RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

25 RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an
 30 evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999,

Trends Genet., 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response though a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237). As such, siRNA molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA.

5 Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown

10 that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi

15 activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA

20 (Nykanen *et al.*, 2001, *Cell*, 107, 309); however, siRNA molecules lacking a 5'-phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using

25 automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous

30 delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.*, International PCT Publication No. WO 99/54459, Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.*, 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μ mol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 second coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μ mol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M = 6.6 μ mol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M = 15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μ L of 0.11 M = 4.4 μ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μ L of 0.25 M = 10 μ mol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aqueous methylamine (1 mL) at 65 °C for 10 minutes. After cooling to –20 °C, the supernatant is removed from the polymer support.

- 5 The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 µL of 0.25 M = 15 µmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis

Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

- 5 Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of
10 EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C.
15 After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 minutes. The vial is brought to room temperature TEA•3HF (0.1 mL) is added and the vial is
20 heated at 65 °C for 15 minutes. The sample is cooled at –20 °C and then quenched with 1.5 M NH₄HCO₃.

For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is
25 detritylated with 0.5% TFA for 13 minutes. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that
30 the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.*,
 5 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.*, 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a
 10 cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as
 15 described herein can also be readily adapted to large scale synthesis platforms employing batch reactors, synthesis columns and the like.

A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

20 The nucleic acid molecules of the present invention can be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high
 25 pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*, the totality of which is hereby incorporated herein by reference) and re-suspended in water.

In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed
 30 based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as

described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar
 5 and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken *et al.*, 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication
 10 No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.*, U.S. Pat. No. 6,300,074; and Burgin *et al.*, *supra*; all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid
 15 molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are
 20 modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS*. 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been
 25 extensively described in the art (see Eckstein *et al.*, International Publication PCT No. WO 92/07065; Perrault *et al.* *Nature*, 1990, 344, 565-568; Pieken *et al.* *Science*, 1991, 253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman *et al.* International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman *et al.*, 1995, *J. Biol. Chem.*, 270, 25702; Beigelman *et al.*,
 30 International PCT publication No. WO 97/26270; Beigelman *et al.*, U.S. Pat. No. 5,716,824; Usman *et al.*, U.S. Pat. No. 5,627,053; Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on

April 20, 1998; Karpeisky *et al.*, 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such

5 publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to

10 promote RNAi in cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide

15 linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more

20 resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to

25 days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

30 In one embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp

nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in
5 substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1,
10 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.*, International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to
15 facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel
20 conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, cholesterol, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either
25 individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active
30 molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

The term "biodegradable linker" as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, cholesterol, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

5 Therapeutic nucleic acid molecules (*e.g.*, siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules
10 described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

 In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such
15 nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

 Use of the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple siNA molecules targeted to different genes; nucleic acid molecules
20 coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and
25 aptamers.

 In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'- cap structure, for example on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

 By "cap structure" is meant chemical modifications, which have been incorporated
30 at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No.

5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap includes, but is not limited to, glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety.

15 Non-limiting examples of the 3'-cap include, but are not limited to, glyceryl, inverted deoxy abasic residue (moiety), 4', 5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol
20 nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate,
25 phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units,
30 including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not

contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12
 5 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain,
 10 branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂, halogen, N(CH₃)₂, amino, or SH. The term "alkyl" also includes alkynyl groups that have an
 15 unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O,
 20 =S, NO₂ or N(CH₃)₂, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The
 25 preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl
 30 groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl

pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417, and Mesmaeker *et al.*, 1994, *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.*, U.S. Pat. No. 5,998,203.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH₂ or 2'-O- NH₂, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro*, stability, and ease of introduction of such oligonucleotides to the target site, *e.g.*, to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Nucleic Acid Molecules

A siNA molecule of the invention can be adapted for use to treat, for example, tumor angiogenesis and cancer, including but not limited to breast cancer, lung cancer (including non-small cell lung carcinoma), prostate cancer, colorectal cancer, brain cancer, esophageal cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck cancer, skin cancers, nasopharyngeal carcinoma, liposarcoma, epithelial carcinoma, renal cell carcinoma, gallbladder adeno carcinoma, parotid adenocarcinoma, ovarian cancer, melanoma, lymphoma, glioma, endometrial sarcoma, multidrug resistant cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, endometriosis, female reproduction, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber

syndrome, Osler-Weber-Rendu syndrome, renal disease such as Autosomal dominant polycystic kidney disease (ADPKD), and any other diseases or conditions that are related to or will respond to the levels of VEGF, VEGFr1, VEGFr2 and/or VEGFr3 in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can

5 comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer *et al.*, 1999, *Mol. Membr. Biol.*,

10 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee *et al.*, 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.*, U.S. Pat. No. 6,395,713 and Sullivan *et al.*, PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule.

15 Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as biodegradable polymers, hydrogels, cyclodextrins (see for example Gonzalez *et al.*, 1999, *Bioconjugate Chem.*, 10, 1068-1074; Wang *et al.*, International PCT publication Nos. WO 03/47518 and WO

20 03/46185), poly(lactic-co-glycolic)acid (PLGA) and PLCA microspheres (see for example US Patent 6,447,796 and US Patent Application Publication No. US 2002130430), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). Alternatively, the nucleic acid/vehicle combination is locally delivered by

25 direct injection or by use of an infusion pump. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can take place using standard needle and syringe methodologies, or by needle-free technologies such as those described in Conry *et al.*, 1999, *Clin. Cancer Res.*, 5, 2330-2337 and Barry *et al.*, International PCT Publication No. WO 99/31262. The molecules

30 of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

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In one embodiment, a compound, molecule, or composition for the treatment of ocular conditions (e.g., macular degeneration, diabetic retinopathy etc.) is administered to a subject intraocularly or by intraocular means. In another embodiment, a compound, molecule, or composition for the treatment of ocular conditions (e.g., macular degeneration, diabetic retinopathy etc.) is administered to a subject periocularly or by periocular means (see for example Ahlheim et al., International PCT publication No. WO 03/24420). In one embodiment, a siNA molecule and/or formulation or composition thereof is administered to a subject intraocularly or by intraocular means. In another embodiment, a siNA molecule and/or formulation or composition thereof is administered to a subject periocularly or by periocular means. Periocular administration generally provides a less invasive approach to administering siNA molecules and formulation or composition thereof to a subject (see for example Ahlheim et al., International PCT publication No. WO 03/24420). The use of periocular administration also minimizes the risk of retinal detachment, allows for more frequent dosing or administration, provides a clinically relevant route of administration for macular degeneration and other optic conditions, and also provides the possibility of using reservoirs (e.g., implants, pumps or other devices) for drug delivery.

In one embodiment, a siNA molecule of the invention is complexed with membrane disruptive agents such as those described in U.S. Patent Application Publication No. 20010007666, incorporated by reference herein in its entirety including the drawings. In another embodiment, the membrane disruptive agent or agents and the siNA molecule are also complexed with a cationic lipid or helper lipid molecule, such as those lipids described in U.S. Patent No. 6,235,310, incorporated by reference herein in its entirety including the drawings.

Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (e.g., RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as tablets, capsules or elixirs for oral administration, suppositories for rectal administration,

sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, 5 e.g., acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, e.g., systemic administration, into a cell or subject, including for example a human. Suitable forms, in part, depend upon the 10 use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that 15 prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and 20 intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of 25 the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess VEGF and/or VEGFr.

30 By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the

instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Jolliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF *et al.*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al., Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 270, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a

greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (*e.g.*, intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches,

lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropylmethylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with

partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above.

The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils
5 are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be
10 prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a
15 sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about
20 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular subject depends upon
25 a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the
30 animal feed or drinking water. It can be convenient to formulate the animal feed and

drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

5 The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

10 In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly
15 depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biantennary or monoantennary chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly *et al.*, 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety,
20 which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.*, 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach
25 to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such
30 bioconjugates are described in Vargeese *et al.*, USSN 10/201,394, filed August 13, 2001; and Matulic-Adamic *et al.*, USSN 10/151,116, filed May 17, 2002. In one embodiment, nucleic acid molecules of the invention are complexed with or covalently attached to

nanoparticles, such as Hepatitis B virus S, M, or L envelope proteins (see for example Yamado *et al.*, 2003, *Nature Biotechnology*, 21, 885). In one embodiment, nucleic acid molecules of the invention are delivered with specificity for human tumor cells, specifically non-apoptotic human tumor cells including for example T-cells, hepatocytes, breast carcinoma cells, ovarian carcinoma cells, melanoma cells, intestinal epithelial cells, prostate cells, testicular cells, non-small cell lung cancers, small cell lung cancers, etc.

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J. Virol.*, 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science*, 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol. Chem.*, 269, 25856.

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly

administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); and c) a nucleic acid sequence encoding at least one of the siNA molecules of the instant invention, wherein said sequence is operably linked to said initiation region and said termination region in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the invention; and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990,

Proc. Natl. Acad. Sci. U S A, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber *et al.*, 1993, *Methods Enzymol.*, 217, 47-66; Zhou *et al.*, 1990, *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.*, 1993, *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992, *EMBO J.*, 11, 4411-8; Lisiewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A*, 90, 8000-4; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson *et al.*, *supra*; Couture and Stinchcomb, 1996, *supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, U.S. Pat. No. 5,624,803; Good *et al.*, 1997, *Gene Ther.*, 4, 45; Beigelman *et al.*, International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, *supra*).

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the

termination region in a manner that allows expression and/or delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

VEGF/VEGFr biology and biochemistry

The following discussion is adapted from R&D Systems, Cytokine Mini Reviews, Vascular Endothelial Growth Factor (VEGF), Copyright ©2002 R&D Systems. Angiogenesis is a process of new blood vessel development from pre-existing vasculature. It plays an essential role in embryonic development, normal growth of tissues, wound healing, the female reproductive cycle (i.e., ovulation, menstruation and placental development), as well as a major role in many diseases. Particular interest has focused on cancer, since tumors cannot grow beyond a few millimeters in size without developing a new blood supply. Angiogenesis is also necessary for the spread and growth of tumor cell metastases.

One of the most important growth and survival factors for endothelium is vascular endothelial growth factor (VEGF). VEGF induces angiogenesis and endothelial cell proliferation and plays an important role in regulating vasculogenesis. VEGF is a heparin-binding glycoprotein that is secreted as a homodimer of 45 kDa. Most types of cells, but usually not endothelial cells themselves, secrete VEGF. Since the initially discovered VEGF, VEGF-A, increases vascular permeability, it was known as vascular permeability factor. In addition, VEGF causes vasodilatation, partly through stimulation

of nitric oxide synthase in endothelial cells. VEGF can also stimulate cell migration and inhibit apoptosis.

There are several splice variants of VEGF-A. The major ones include: 121, 165, 189 and 206 amino acids (aa), each one comprising a specific exon addition. VEGF165 is the most predominant protein, but transcripts of VEGF 121 may be more abundant. VEGF206 is rarely expressed and has been detected only in fetal liver. Recently, other splice variants of 145 and 183 aa have also been described. The 165, 189 and 206 aa splice variants have heparin-binding domains, which help anchor them in extracellular matrix and are involved in binding to heparin sulfate and presentation to VEGF receptors. Such presentation is a key factor for VEGF potency (i.e., the heparin-binding forms are more active). Several other members of the VEGF family have been cloned including VEGF-B, -C, and -D. Placenta growth factor (PlGF) is also closely related to VEGF-A. VEGF-A, -B, -C, -D, and PlGF are all distantly related to platelet-derived growth factors-A and -B. Less is known about the function and regulation of VEGF-B, -C, and -D, but they do not seem to be regulated by the major pathways that regulate VEGF-A.

VEGF-A transcription is potentiated in response to hypoxia and by activated oncogenes. The transcription factors, hypoxia inducible factor-1a (hif-1a) and -2a, are degraded by proteosomes in normoxia and stabilized in hypoxia. This pathway is dependent on the Von Hippel-Lindau gene product. Hif-1a and hif-2 a heterodimerize with the aryl hydrocarbon nuclear translocator in the nucleus and bind the VEGF promoter/enhancer. This is a key pathway expressed in most types of cells. Hypoxia inducibility, in particular, characterizes VEGF-A versus other members of the VEGF family and other angiogenic factors. VEGF transcription in normoxia is activated by many oncogenes, including H-ras and several transmembrane tyrosine kinases, such as the epidermal growth factor receptor and erbB2. These pathways together account for a marked upregulation of VEGF-A in tumors compared to normal tissues and are often of prognostic importance.

There are three receptors in the VEGF receptor family. They have the common properties of multiple IgG-like extracellular domains and tyrosine kinase activity. The enzyme domains of VEGF receptor 1 (VEGFr1, also known as Flt-1), VEGFr2 (also

known as KDR or Flk-1), and VEGFr3 (also known as Flt-4) are divided by an inserted sequence. Endothelial cells also express additional VEGF receptors, Neuropilin-1 and Neuropilin-2. VEGF-A binds to VEGFr1 and VEGFr2 and to Neuropilin-1 and Neuropilin-2. PlGF and VEGF-B bind VEGFr1 and Neuropilin-1. VEGF-C and -D bind
 5 VEGFr3 and VEGFr2.

The VEGF-C/VEGFr3 pathway is important for lymphatic proliferation. VEGFr3 is specifically expressed on lymphatic endothelium. A soluble form of Flt-1 can be detected in peripheral blood and is a high affinity ligand for VEGF. Soluble Flt-1 can be used to antagonize VEGF function. VEGFr1 and VEGFr2 are upregulated in tumor and
 10 proliferating endothelium, partly by hypoxia and also in response to VEGF-A itself. VEGFr1 and VEGFr2 can interact with multiple downstream signaling pathways via proteins such as PLC-g, Ras, Shc, Nck, PKC and PI3-kinase. VEGFr1 is of higher affinity than VEGFr2 and mediates motility and vascular permeability. VEGFr2 is necessary for proliferation.

15 VEGF can be detected in both plasma and serum samples of patients, with much higher levels in serum. Platelets release VEGF upon aggregation and may be a major source of VEGF delivery to tumors. Several studies have shown that association of high serum levels of VEGF with poor prognosis in cancer patients may be correlated with an elevated platelet count. Many tumors release cytokines that can stimulate the production
 20 of megakaryocytes in the marrow and elevate the platelet count. This can result in an indirect increase of VEGF delivery to tumors.

VEGF is implicated in several other pathological conditions associated with enhanced angiogenesis. For example, VEGF plays a role in both psoriasis and rheumatoid arthritis. Diabetic retinopathy is associated with high intraocular levels of
 25 VEGF. Inhibition of VEGF function may result in infertility by blockade of corpus luteum function. Direct demonstration of the importance of VEGF in tumor growth has been achieved using dominant negative VEGF receptors to block in vivo proliferation, as well as blocking antibodies to VEGF39 or to VEGFr2.

The use of small interfering nucleic acid molecules targeting VEGF and
 30 corresponding receptors and ligands therefore provides a class of novel therapeutic agents that can be used in the diagnosis of and the treatment of cancer, proliferative

diseases, or any other disease or condition that responds to modulation of VEGF and/or VEGFr genes.

Examples:

The following are non-limiting examples showing the selection, isolation,
5 synthesis and activity of nucleic acids of the instant invention.

Example 1: Tandem synthesis of siNA constructs

Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example, a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in
10 high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the
15 oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even
20 though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example, by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of
25 introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is
30 coupled, standard synthesis chemistry is utilized to complete synthesis of the second

sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M $\text{NH}_4\text{H}_2\text{CO}_3$.

Purification of the siNA duplex can be readily accomplished using solid phase
 5 extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1
 column volume (CV) of acetonitrile, 2 CV H_2O , and 2 CV 50mM NaOAc. The sample
 is loaded and then washed with 1 CV H_2O or 50mM NaOAc. Failure sequences are
 eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The
 column is then washed, for example with 1 CV H_2O followed by on-column
 10 detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA)
 over the column, then adding a second CV of 1% aqueous TFA to the column and
 allowing to stand for approximately 10 minutes. The remaining TFA solution is
 removed and the column washed with H_2O followed by 1 CV 1M NaCl and additional
 H_2O . The siNA duplex product is then eluted, for example, using 1 CV 20% aqueous
 15 CAN.

Figure 2 provides an example of MALDI-TOF mass spectrometry analysis of a
 purified siNA construct in which each peak corresponds to the calculated mass of an
 individual siNA strand of the siNA duplex. The same purified siNA provides three
 peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably
 20 corresponding to the duplex siNA, and two peaks presumably corresponding to the
 separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA contract
 only shows a single peak. Testing of the purified siNA construct using a luciferase
 reporter assay described below demonstrated the same RNAi activity compared to siNA
 constructs generated from separately synthesized oligonucleotide sequence strands.

25 Example 2: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA
 transcript, is screened for target sites, for example by using a computer folding
 algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript
 derived from a database, such as Genbank, is used to generate siNA targets having
 30 complementarity to the target. Such sequences can be obtained from a database, or can
 be determined experimentally as known in the art. Target sites that are known, for

example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

Example 3: Selection of siNA molecule target sites in a RNA

The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

1. The target sequence is parsed *in silico* into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.
2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences

that are present in most or all of the target sequences. Alternately, the ranking can identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.

- 5 3. In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene
10 but are absent in the untargeted paralog.
4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.
- 15 5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.
- 20 6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.
- 25 7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.
- 30 8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper

(sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see **Tables II and III**). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.

9. The siNA molecules are screened in an *in vitro*, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

10 In an alternate approach, a pool of siNA constructs specific to a VEGF and/or VEGFr target sequence is used to screen for target sites in cells expressing VEGF and/or VEGFr RNA, such as HUVEC, HMVEC, or A375 cells. The general strategy used in this approach is shown in **Figure 9**. A non-limiting example of such is a pool comprising sequences having any of SEQ ID NOS 1-2455. Cells expressing VEGF and/or VEGFr (e.g., HUVEC, HMVEC, or A375 cells) are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with VEGF and/or VEGFr inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example **Figure 7** and **Figure 8**). The siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation, decreased VEGF and/or VEGFr mRNA levels or decreased VEGF and/or VEGFr protein expression), are sequenced to determine the most suitable target site(s) within the target VEGF and/or VEGFr RNA sequence.

Example 4: VEGF and/or VEGFr targeted siNA design

siNA target sites were chosen by analyzing sequences of the VEGF and/or VEGFr RNA target and optionally prioritizing the target sites on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 3, or alternately by using an *in vitro* siNA system as described in Example 6 herein. siNA molecules were designed that could bind each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of the siNA molecules can be chosen to optimize activity. Generally, a sufficient

number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 11**).

Example 5: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.*, US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.*, US Patent Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoroamidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O-Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.*, US Patent 5,631,360, incorporated by reference herein in its entirety).

During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'-direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5'-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency, for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Deprotection and purification of the siNA can be performed as is generally described in Usman *et al.*, US 5,831,071, US 6,353,098, US 6,437,117, and Bellon *et al.*, US 6,054,576, US 6,162,909, US 6,303,773, or Scaringe *supra*, incorporated by reference herein in their entireties. Additionally, deprotection conditions can be

modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-
 5 2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

Example 6: RNAi *in vitro* assay to assess siNA activity

An *in vitro* assay that recapitulates RNAi in a cell-free system is used to evaluate
 10 siNA constructs targeting VEGF and/or VEGFr RNA targets. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with VEGF and/or VEGFr target RNA. A *Drosophila* extract derived from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*. Target RNA is generated via *in vitro* transcription from an
 15 appropriate VEGF and/or VEGFr expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 minute at 90°C followed by 1 hour at 37°C, then diluted in lysis buffer (for example 100 mM potassium acetate, 30
 20 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate). Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The assay comprises a reaction mixture
 25 containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug.ml creatine phosphokinase, 100 uM GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final concentration of potassium acetate is adjusted to 100
 30 mM. The reactions are pre-assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25 x Passive Lysis Buffer (Promega). Target RNA

cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [α - 32 P] CTP, passed over a G 50 Sephadex column
 5 by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'- 32 P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands
 10 representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

In one embodiment, this assay is used to determine target sites the VEGF and/or VEGFr RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the VEGF and/or VEGFr RNA
 15 target, for example, by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

Example 7: Nucleic acid inhibition of VEGF and/or VEGFr target RNA *in vivo*

siNA molecules targeted to the human VEGF and/or VEGFr RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for
 20 cleavage activity *in vivo*, for example, using the following procedure. The target sequences and the nucleotide location within the VEGF and/or VEGFr RNA are given in **Table II and III**.

Two formats are used to test the efficacy of siNAs targeting VEGF and/or VEGFr. First, the reagents are tested in cell culture using, for example, HUVEC, HMVEC, or
 25 A375 cells to determine the extent of RNA and protein inhibition. siNA reagents (*e.g.*; see **Tables II and III**) are selected against the VEGF and/or VEGFr target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example, HUVEC, HMVEC, or A375 cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of
 30 amplification (*eg.*, ABI 7700 Taqman[®]). A comparison is made to a mixture of

oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-
 5 course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

Delivery of siNA to Cells

Cells (e.g., HUVEC, HMVEC, or A375 cells) are seeded, for example, at 1×10^5 cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20nM) and cationic lipid (e.g., final concentration
 10 $2 \mu\text{g/ml}$) are complexed in EGM basal media (Biowhittaker) at 37°C for 30 minutes in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at 1×10^3 in 96 well plates and siNA complex added as described. Efficiency
 15 of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

Taqman and Lightcycler quantification of mRNA

20 Total RNA is prepared from cells following siNA delivery, for example, using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For Taqman analysis, dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM
 25 7700 Sequence Detector using 50 μl reactions consisting of 10 μl total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM MgCl_2 , 300 μM each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AmpliTaq Gold (PE-Applied Biosystems) and 10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can
 30 consist of 30 minutes at 48°C , 10 minutes at 95°C , followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C . Quantitation of mRNA levels is determined relative to

standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/rxn) and normalizing to β -actin or GAPDH mRNA in parallel TaqMan reactions. For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of SYBR Green I dye into a specific PCR product can
 5 be measured in glass capillary tubes using a lightcycler. A standard curve is generated for each primer pair using control cRNA. Values are represented as relative expression to GAPDH in each sample.

Western blotting

Nuclear extracts can be prepared using a standard micro preparation technique (see
 10 for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage
 15 (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with
 20 SuperSignal reagent (Pierce).

Example 8: Animal Models useful to evaluate the down-regulation of VEGF and/or VEGFr gene expression

There are several animal models in which the anti-angiogenesis effect of nucleic acids of the present invention, such as siRNA, directed against VEGF, VEGFr1, VEGFr2
 25 and/or VEGFr3 mRNAs can be tested. Typically a corneal model has been used to study angiogenesis in rat and rabbit since recruitment of vessels can easily be followed in this normally avascular tissue (Pandey *et al.*, 1995 *Science* 268: 567-569). In these models, a small Teflon or Hydrion disk pretreated with an angiogenesis factor (e.g. bFGF or VEGF) is inserted into a pocket surgically created in the cornea. Angiogenesis is
 30 monitored 3 to 5 days later. siRNA directed against VEGF, VEGFr1, VEGFr2 and/or VEGFr3 mRNAs are delivered in the disk as well, or dropwise to the eye over the time

course of the experiment. In another eye model, hypoxia has been shown to cause both increased expression of VEGF and neovascularization in the retina (Pierce *et al.*, 1995 *Proc. Natl. Acad. Sci. USA.* 92: 905-909; Shweiki *et al.*, 1992 *J. Clin. Invest.* 91: 2235-2243).

5 In human glioblastomas, it has been shown that VEGF is at least partially responsible for tumor angiogenesis (Plate *et al.*, 1992 *Nature* 359, 845). Animal models have been developed in which glioblastoma cells are implanted subcutaneously into nude mice and the progress of tumor growth and angiogenesis is studied (Kim *et al.*, 1993 *supra*; Millauer *et al.*, 1994 *supra*).

10 Another animal model that addresses neovascularization involves Matrigel, an extract of basement membrane that becomes a solid gel when injected subcutaneously (Passaniti *et al.*, 1992 *Lab. Invest.* 67: 519-528). When the Matrigel is supplemented with angiogenesis factors such as VEGF, vessels grow into the Matrigel over a period of 3 to 5 days and angiogenesis can be assessed. Again, nucleic acids directed against
15 VEGFr mRNAs are delivered in the Matrigel.

Several animal models exist for screening of anti-angiogenic agents. These include corneal vessel formation following corneal injury (Burger *et al.*, 1985 *Cornea* 4: 35-41; Lepri, *et al.*, 1994 *J. Ocular Pharmacol.* 10: 273-280; Ormerod *et al.*, 1990 *Am. J. Pathol.* 137: 1243-1252) or intracorneal growth factor implant (Grant *et al.*, 1993
20 *Diabetologia* 36: 282-291; Pandey *et al.* 1995 *supra*; Zieche *et al.*, 1992 *Lab. Invest.* 67: 711-715), vessel growth into Matrigel matrix containing growth factors (Passaniti *et al.*, 1992 *supra*), female reproductive organ neovascularization following hormonal manipulation (Shweiki *et al.*, 1993 *Clin. Invest.* 91: 2235-2243), several models involving inhibition of tumor growth in highly vascularized solid tumors (O'Reilly *et al.*,
25 1994 *Cell* 79: 315-328; Senger *et al.*, 1993 *Cancer and Metas. Rev.* 12: 303-324; Takahasi *et al.*, 1994 *Cancer Res.* 54: 4233-4237; Kim *et al.*, 1993 *supra*), and transient hypoxia-induced neovascularization in the mouse retina (Pierce *et al.*, 1995 *Proc. Natl. Acad. Sci. USA.* 92: 905-909). Other model systems to study tumor angiogenesis are reviewed by Folkman, 1985 *Adv. Cancer. Res.* 43, 175.

30 *Ocular Models of Angiogenesis*

The cornea model, described in Pandey *et al. supra*, is the most common and well characterized model for screening anti-angiogenic agent efficacy. This model involves an avascular tissue into which vessels are recruited by a stimulating agent (growth factor, thermal or alkalai burn, endotoxin). The corneal model utilizes the intrastromal corneal
 5 implantation of a Teflon pellet soaked in a VEGF-Hydron solution to recruit blood vessels toward the pellet, which can be quantitated using standard microscopic and image analysis techniques. To evaluate their anti-angiogenic efficacy, nucleic acids are applied topically to the eye or bound within Hydron on the Teflon pellet itself. This avascular cornea as well as the Matrigel (see below) provide for low background assays.
 10 While the corneal model has been performed extensively in the rabbit, studies in the rat have also been conducted.

The mouse model (Passaniti *et al., supra*) is a non-tissue model that utilizes Matrigel, an extract of basement membrane (Kleinman *et al.*, 1986) or Millipore® filter disk, which can be impregnated with growth factors and anti-angiogenic agents in a
 15 liquid form prior to injection. Upon subcutaneous administration at body temperature, the Matrigel or Millipore® filter disk forms a solid implant. VEGF embedded in the Matrigel or Millipore® filter disk is used to recruit vessels within the matrix of the Matrigel or Millipore® filter disk which can be processed histologically for endothelial cell specific vWF (factor VIII antigen) immunohistochemistry, Trichrome-Masson stain,
 20 or hemoglobin content. Like the cornea, the Matrigel or Millipore® filter disk is avascular; however, it is not tissue. In the Matrigel or Millipore® filter disk model, nucleic acids are administered within the matrix of the Matrigel or Millipore® filter disk to test their anti-angiogenic efficacy. Thus, delivery issues in this model, as with delivery of nucleic acids by Hydron- coated Teflon pellets in the rat cornea model, may
 25 be less problematic due to the homogeneous presence of the nucleic acid within the respective matrix.

Additionally, siNA molecules of the invention targeting VEGF and/or VEGFr (e.g. VEGFR1, VEGFR2, and/or VEGFR3) can be assessed for activity transgenic mice to determine whether modulation of VEGF and/or VEGFr can inhibit optic
 30 neovascularization. Animal models of choroidal neovascularization are described in, for example, Mori *et al.*, 2001, *Journal of Cellular Physiology*, 188, 253; Mori *et al.*, 2001,

American Journal of Pathology, 159, 313; Ohno-Matsui et al., 2002, *American Journal of Pathology*, 160, 711; and Kwak et al., 2000, *Investigative Ophthalmology & Visual Science*, 41, 3158. VEGF plays a central role in causing retinal neovascularization. Increased expression of VEGFR2 in retinal photoreceptors of transgenic mice stimulates
 5 neovascularization within the retina, and a blockade of VEGFR2 signaling has been shown to inhibit retinal choroidal neovascularization (CNV) (Mori et al., 2001, *J. Cell. Physiol.*, 188, 253).

CNV is laser induced in, for example, adult C57BL/6 mice. The mice are also given an intravitreal, periocular or a subretinal injection of VEGF and/or VEGFr (e.g.,
 10 VEGFR2) siNA in each eye. Intravitreal injections are made using a Harvard pump microinjection apparatus and pulled glass micropipets. Then a micropipette is passed through the sclera just behind the limbus into the vitreal cavity. The subretinal injections are made using a condensing lens system on a dissecting microscope. The pipet tip is then passed through the sclera posterior to the limbus and positioned above
 15 the retina. Five days after the injection of the vector the mice are anesthetized with ketamine hydrochloride (100 mg/kg body weight), 1% tropicamide is also used to dilate the pupil, and a diode laser photocoagulation is used to rupture Bruch's membrane at three locations in each eye. A slit lamp delivery system and a hand-held cover slide are used for laser photocoagulation. Burns are made in the 9, 12, and 3 o'clock positions 2-3
 20 disc diameters from the optic nerve (Mori et al., *supra*).

The mice typically develop subretinal neovascularization due to the expression of VEGF in photoreceptors beginning at prenatal day 7. At prenatal day 21, the mice are anesthetized and perfused with 1 ml of phosphate-buffered saline containing 50 mg/ml of fluorescein-labeled dextran. Then the eyes are removed and placed for 1 hour in a 10%
 25 phosphate-buffered formalin. The retinas are removed and examined by fluorescence microscopy (Mori et al., *supra*).

Fourteen days after the laser induced rupture of Bruch's membrane, the eyes that received intravitreal and subretinal injection of siNA are evaluated for smaller appearing areas of CNV, while control eyes are evaluated for large areas of CNV. The
 30 eyes that receive intravitreal injections or a subretinal injection of siNA are also evaluated for fewer areas of neovascularization on the outer surface of the retina and

potencial abortive sprouts from deep retinal capillaries that do not reach the retinal surface compared to eyes that did not receive an injection of siNA.

Tumor Models of Angiogenesis

Use of murine models

- 5 For a typical systemic study involving 10 mice (20 g each) per dose group, 5 doses (1, 3, 10, 30 and 100 mg/kg daily over 14 days continuous administration), approximately 400 mg of siRNA, formulated in saline is used. A similar study in young adult rats (200 g) requires over 4 g. Parallel pharmacokinetic studies involve the use of similar quantities of siRNA further justifying the use of murine models.

10 *Lewis lung carcinoma and B-16 melanoma murine models*

Identifying a common animal model for systemic efficacy testing of nucleic acids is an efficient way of screening siRNA for systemic efficacy.

- 15 The Lewis lung carcinoma and B-16 murine melanoma models are well accepted models of primary and metastatic cancer and are used for initial screening of anti-cancer agents. These murine models are not dependent upon the use of immunodeficient mice, are relatively inexpensive, and minimize housing concerns. Both the Lewis lung and B-16 melanoma models involve subcutaneous implantation of approximately 10^6 tumor cells from metastatically aggressive tumor cell lines (Lewis lung lines 3LL or D122, LLc-LN7; B-16-BL6 melanoma) in C57BL/6J mice. Alternatively, the Lewis lung
- 20 model can be produced by the surgical implantation of tumor spheres (approximately 0.8 mm in diameter). Metastasis also can be modeled by injecting the tumor cells directly intravenously. In the Lewis lung model, microscopic metastases can be observed approximately 14 days following implantation with quantifiable macroscopic metastatic tumors developing within 21-25 days. The B-16 melanoma exhibits a similar time course
- 25 with tumor neovascularization beginning 4 days following implantation. Since both primary and metastatic tumors exist in these models after 21-25 days in the same animal, multiple measurements can be taken as indices of efficacy. Primary tumor volume and growth latency as well as the number of micro- and macroscopic metastatic lung foci or number of animals exhibiting metastases can be quantitated. The percent increase in
- 30 lifespan can also be measured. Thus, these models provide suitable primary efficacy

assays for screening systemically administered siRNA nucleic acids and siRNA nucleic acid formulations.

In the Lewis lung and B-16 melanoma models, systemic pharmacotherapy with a wide variety of agents usually begins 1-7 days following tumor implantation/inoculation with either continuous or multiple administration regimens. Concurrent pharmacokinetic studies can be performed to determine whether sufficient tissue levels of siRNA can be achieved for pharmacodynamic effect to be expected. Furthermore, primary tumors and secondary lung metastases can be removed and subjected to a variety of *in vitro* studies (*i.e.* target RNA reduction).

In addition, animal models are useful in screening compounds, eg. siRNA molecules, for efficacy in treating renal failure, such as a result of autosomal dominant polycystic kidney disease (ADPKD). The Han:SPRD rat model, mice with a targeted mutation in the Pkd2 gene and congenital polycystic kidney (cpk) mice, closely resemble human ADPKD and provide animal models to evaluate the therapeutic effect of siRNA constructs that have the potential to interfere with one or more of the pathogenic elements of ADPKD mediated renal failure, such as angiogenesis. Angiogenesis may be necessary in the progression of ADPKD for growth of cyst cells as well as increased vascular permeability promoting fluid secretion into cysts. Proliferation of cystic epithelium is also a feature of ADPKD because cyst cells in culture produce soluble vascular endothelial growth factor (VEGF). VEGFr1 has also been detected in epithelial cells of cystic tubules but not in endothelial cells in the vasculature of cystic kidneys or normal kidneys. VEGFr2 expression is increased in endothelial cells of cyst vessels and in endothelial cells during renal ischemia-reperfusion. It is proposed that inhibition of VEGF receptors with anti-VEGFr1 and anti-VEGFr2 siRNA molecules would attenuate cyst formation, renal failure and mortality in ADPKD. Anti-VEGFr2 siRNA molecules would therefore be designed to inhibit angiogenesis involved in cyst formation. As VEGFr1 is present in cystic epithelium and not in vascular endothelium of cysts, it is proposed that anti-VEGFr1 siRNA molecules would attenuate cystic epithelial cell proliferation and apoptosis which would in turn lead to less cyst formation. Further, it is proposed that VEGF produced by cystic epithelial cells is one of the stimuli for angiogenesis as well as epithelial cell proliferation and apoptosis. The use of Han:SPRD rats (see for example Kaspareit-Rittinghausen *et al.*, 1991, *Am.J.Pathol.* 139, 693-696),

mice with a targeted mutation in the *Pkd2* gene (*Pkd2*^{-/-} mice, see for example Wu *et al.*, 2000, *Nat. Genet.* 24, 75-78) and *cpk* mice (see for example Woo *et al.*, 1994, *Nature*, 368, 750-753) all provide animal models to study the efficacy of siRNA molecules of the invention against VEGFr1 and VEGFr2 mediated renal failure.

5 VEGF, VEGFr1 VEGFR2 and/or VEGFr3 protein levels can be measured clinically or experimentally by FACS analysis. VEGF, VEGFr1 VEGFR2 and/or VEGFr3 encoded mRNA levels are assessed by Northern analysis, RNase-protection, primer extension analysis and/or quantitative RT-PCR. siRNA nucleic acids that block VEGF, VEGFr1 VEGFR2 and/or VEGFr3 protein encoding mRNAs and therefore result in decreased
10 levels of VEGF, VEGFr1 VEGFR2 and/or VEGFr3 activity by more than 20% *in vitro* can be identified.

Example 9: RNAi mediated inhibition of VEGFr1 RNA expression

siNA constructs (Table III) are tested for efficacy in reducing VEGF and/or VEGFr RNA expression in, for example, HUVEC, HMVEC, or A375 cells. Cells are
15 plated approximately 24 hours before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA
20 concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well.
25 Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs is determined.

30 **Figure 13** shows a non-limiting example of reduction of VEGFr1 mRNA in A375 cells mediated by chemically-modified siNAs that target VEGFr1 mRNA. A549 cells

were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs (Stabilization “Stab” chemistries are shown in **Table IV**, constructs are referred to by RPI number, see **Table III**) comprising Stab 4/5 chemistry (Sirna/RPI 31190/31193), Stab 1/2 chemistry (Sirna/RPI 31183/31186 and Sirna/RPI 31184/31187),
 5 and unmodified RNA (Sirna/RPI 30075/30076) were compared to untreated cells, matched chemistry inverted control siNA constructs (Sirna/RPI 31208/31211, Sirna/RPI 31201/31204, Sirna/RPI 31202/31205, and Sirna/RPI 30077/30078), scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, all of the siNA constructs significantly
 10 reduce VEGFr1 RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control).

15 Example 10: siNA-mediated inhibition of angiogenesis *in vivo*

Evaluation of siNA molecules in the rat cornea model of VEGF induced angiogenesis

The purpose of this study was to assess the anti-angiogenic activity of siNA targeted against VEGFR1, using the rat cornea model of VEGF induced angiogenesis. The siNA molecules referred to in **Figure 12** have matched inverted controls which are
 20 inactive since they are not able to interact with the RNA target. The siNA molecules and VEGF were co-delivered using the filter disk method. Nitrocellulose filter disks (Millipore®) of 0.057 diameter were immersed in appropriate solutions and were surgically implanted in rat cornea as described by Pandey *et al.*, *supra*.

The stimulus for angiogenesis in this study was the treatment of the filter disk with
 25 30 µM VEGF, which is implanted within the cornea's stroma. This dose yields reproducible neovascularization stemming from the pericorneal vascular plexus growing toward the disk in a dose-response study 5 days following implant. Filter disks treated only with the vehicle for VEGF show no angiogenic response. The siNA were co-administered with VEGF on a disk in three different siNA concentrations. One concern
 30 with the simultaneous administration is that the siNA would not be able to inhibit angiogenesis since VEGF receptors can be stimulated. However, Applicant has observed

that in low VEGF doses, the neovascular response reverts to normal suggesting that the VEGF stimulus is essential for maintaining the angiogenic response. Blocking the production of VEGF receptors using simultaneous administration of anti-VEGF-R mRNA siNA could attenuate the normal neovascularization induced by the filter disk
 5 treated with VEGF.

Materials and Methods:

Test Compounds and Controls

R&D Systems VEGF, carrier free at 75 μ M in 82 mM Tris-Cl, pH 6.9
 10 siNA, 1.67 μ G/ μ L, SITE 2340 (SIRNA/RPI 29695/29699) sense/antisense
 siNA, 1.67 μ G/ μ L, INVERTED CONTROL FOR SITE 2340 (SIRNA/RPI
 29983/29984) sense/antisense
 siNA 1.67 μ g/ μ L, Site 2340 (Sirma/RPI 30196/30416) sense/antisense

Animals

15 Harlan Sprague-Dawley Rats, Approximately 225-250g
 45 males, 5 animals per group.

Husbandry

20 Animals are housed in groups of two. Feed, water, temperature and humidity are determined according to Pharmacology Testing Facility performance standards (SOP's) which are in accordance with the 1996 Guide for the Care and Use of Laboratory Animals (NRC). Animals are acclimated to the facility for at least 7 days prior to experimentation. During this time, animals are observed for overall health and sentinels
 25 are bled for baseline serology.

Experimental Groups

Each solution (VEGF and siNAs) was prepared as a 1X solution for final concentrations shown in the experimental groups described in **Table III**.

siNA Annealing Conditions

siNA sense and antisense strands are annealed for 1 minute in H₂O at 1.67mg/mL/strand followed by a 1 hour incubation at 37°C producing 3.34 mg/mL of
 5 duplexed siNA. For the 20µg/eye treatment, 6 µLs of the 3.34 mg/mL duplex is injected into the eye (see below). The 3.34 mg/mL duplex siNA can then be serially diluted for dose response assays.

Preparation of VEGF Filter Disk

10

For corneal implantation, 0.57 mm diameter nitrocellulose disks, prepared from 0.45 µm pore diameter nitrocellulose filter membranes (Millipore Corporation), were soaked for 30 min in 1 µL of 75 µM VEGF in 82 mM Tris-HCl (pH 6.9) in covered petri dishes on ice. Filter disks soaked only with the vehicle for VEGF (83 mM Tris-Cl pH
 15 6.9) elicit no angiogenic response.

Corneal surgery

The rat corneal model used in this study was a modified from Koch *et al. Supra* and Pandey *et al., supra*. Briefly, corneas were irrigated with 0.5% povidone iodine
 20 solution followed by normal saline and two drops of 2% lidocaine. Under a dissecting microscope (Leica MZ-6), a stromal pocket was created and a presoaked filter disk (see above) was inserted into the pocket such that its edge was 1 mm from the corneal limbus.

Intraconjunctival injection of test solutions

25 Immediately after disk insertion, the tip of a 40-50 µm OD injector (constructed in our laboratory) was inserted within the conjunctival tissue 1 mm away from the edge of the corneal limbus that was directly adjacent to the VEGF-soaked filter disk. Six hundred nanoliters of test solution (siNA, inverted control or sterile water vehicle) were dispensed at a rate of 1.2 µL/min using a syringe pump (Kd Scientific). The injector was then
 30 removed, serially rinsed in 70% ethanol and sterile water and immersed in sterile water between each injection. Once the test solution was injected, closure of the eyelid was

maintained using microaneurism clips until the animal began to recover gross motor activity. Following treatment, animals were warmed on a heating pad at 37°C.

Quantitation of angiogenic response

5 Five days after disk implantation, animals were euthanized following administration of 0.4 mg/kg atropine and corneas were digitally imaged. The neovascular surface area (NSA, expressed in pixels) was measured *postmortem* from blood-filled corneal vessels using computerized morphometry (Image Pro Plus, Media Cybernetics, v2.0). The individual mean NSA was determined in triplicate from three regions of
10 identical size in the area of maximal neovascularization between the filter disk and the limbus. The number of pixels corresponding to the blood-filled corneal vessels in these regions was summated to produce an index of NSA. A group mean NSA was then calculated. Data from each treatment group were normalized to VEGF/siNA vehicle-treated control NSA and finally expressed as percent inhibition of VEGF-induced
15 angiogenesis.

Statistics

After determining the normality of treatment group means, group mean percent inhibition of VEGF-induced angiogenesis was subjected to a one-way analysis of
20 variance. This was followed by two post-hoc tests for significance including Dunnett's (comparison to VEGF control) and Tukey-Kramer (all other group mean comparisons) at alpha = 0.05. Statistical analyses were performed using JMP v.3.1.6 (SAS Institute).

Results of the study are graphically represented in **Figures 12 and 16**. As shown in **Figure 12**, VEGFr1 site 4229 active siNA (Sirna/RPI 29695/29699) at three
25 concentrations was effective at inhibiting angiogenesis compared to the inverted siNA control (Sirna/RPI 29983/29984) and the VEGF control. A chemically modified version of the VEGFr1 site 4229 active siNA comprising a sense strand having 2'-deoxy-2'-fluoro pyrimidines and ribo purines with 5' and 3' terminal inverted deoxybasic residues and an antisense strand having having 2'-deoxy-2'-fluoro pyrimidines and ribo
30 purines with a terminal 3'-phosphorothioate internucleotide linkage (Sirna/RPI 30196/30416), showed similar inhibition. Furthermore, VEGFr1 site 349 active siNA

having “Stab 9/10” chemistry (Compound No. 31270/31273) was tested for inhibition of VEGF-induced angiogenesis at three different concentrations (2.0 ug, 1.0 ug, and 0.1 ug dose response) as compared to a matched chemistry inverted control siNA construct (Compound No. 31276/31279) at each concentration and a VEGF control in which no siNA was administered. As shown in **Figure 16**, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is highly effective in inhibiting VEGF-induced angiogenesis in the rat corneal model compared to the matched chemistry inverted control siNA at concentrations from 0.1 ug to 2.0 ug. These results demonstrate that siNA molecules having different chemically modified compositions, such as the modifications described herein, are capable of significantly inhibiting angiogenesis *in vivo*.

Evaluation of siNA molecules in the mouse coroidal model of neovascularization.

Intraocular Administration of siNA

Female C57BL/6 mice (4-5 weeks old) were anesthetized with a 0.2 ml of a mixture of ketamine/xylazine (8:1), and the pupils were dilated with a single drop of 1% tropicamide. Then a 532nm diode laser photocoagulation (75 μ m spot size, 0.1-second duration, 120 mW) was used to generate three laser spots in each eye surrounding the optic nerve by using a hand-held coverslip as a contact lens. A bubble formed at the laser spot indicating a rupture of the Bruch's membrane. Next, the laser spots were evaluated for the presence of CNV on day 17 after laser treatment.

After laser induction of multiple CNV lesions in mice, the siNA was administered by intraocular injections under a dissecting microscope. Intravitreal injections were performed with a Harvard pump microinjection apparatus and pulled glass micropipets. Each micropipet was calibrated to deliver 1 μ L of vehicle containing 0.5 ug or 1.5 ug of siNA, inverted control siNA, or saline. The mice were anesthetized, pupils were dilated, and, the sharpened tip of the micropipet was passed through the sclera, just behind the limbus into the vitreous cavity, and the foot switch was depressed. The injection was repeated at day 7 after laser photocoagulation.

At the time of death, mice were anesthetized (ketamine/xylazine mixture, 8:1) and perfused through the heart with 1 ml PBS containing 50 mg/ml fluorescein-labeled

dextran (FITC-Dextran, 2 million average molecular weight, Sigma). The eyes were removed and fixed for overnight in 1% phosphate-buffered 4% Formalin. The cornea and the lens were removed and the neurosensory retina was carefully dissected from the eyecup. Five radial cuts were made from the edge of the eyecup to the equator; the sclera-choroid-retinal pigment epithelium (RPE) complex was flat-mounted, with the sclera facing down, on a glass slide in Aquamount. Flat mounts were examined with a Nikon fluorescence microscope. A laser spot with green vessels was scored CNV-positive, and a laser spot lacking green vessels was scored CNV-negative. Flatmounts were examined by fluorescence microscopy (Axioskop; Carl Zeiss, Thornwood, NY), and images were digitized with a three-color charge-coupled device (CCD) video camera and a frame grabber. Image-analysis software (Image-Pro Plus; Media Cybernetics, Silver Spring, MD) was used to measure the total area of hyperfluorescence associated with each burn, corresponding to the total fibrovascular scar. The areas within each eye were averaged to give one experimental value per eye for plotting the areas.

Measurement of VEGFr1 expression was also determined using RT-PCR and/or real-time PCR. Retinal RNA was isolated by a Rnaeasy kit, and reverse transcription was performed with approximately 0.5 µg total RNA, reverse transcriptase (SuperScript II), and 5.0 µM oligo-d(T) primer. PCR amplification was performed using primers specific for VEGFR-1 (5'-AAGATGCCAGCCGAAGGAGA-3', SEQ ID NO: 2456) and (5'-GGCTCGGCACCTATAGACA-3', SEQ ID NO: 2457). Titrations were determined to ensure that PCR reactions were performed in the linear range of amplification. Mouse S16 ribosomal protein primers (5'-CACTGCAAACGGGGAAATGG-3', SEQ ID NO: 2458 and 5'-TGAGATGGACTGTCGGATGG-3', SEQ ID NO: 2459) were used to provide an internal control for the amount of template in the PCR reactions.

VEGFr1 site 349 active siNA having "Stab 9/10" chemistry (Compound No. 31270/31273, Table III) was tested for inhibition of VEGF-induced neovascularization at two different concentrations (1.5 ug, and 0.5 ug dose response) as compared to a matched chemistry 1.5 ug inverted control siNA construct (Compound No. 31276/31279, Table III) and a saline control. As shown in **Figure 17**, the active siNA construct having "Stab 9/10" chemistry is highly effective in inhibiting VEGFr1 induced neovascularization (57% inhibition) in the C57BL/6 mice intraocular delivery model compared to the matched chemistry inverted control siNA. The active siNA construct

was also highly effective in inhibiting VEGFr1 induced neovascularization (66% inhibition) compared to the saline control. Additionally, RT-PCR analysis of VEGFr1 site 349 siNA having “Stab 9/10” chemistry (Compound No. 31270/31273, Table III) showed significant reduction in the level of VEGFr1 mRNA compared to the inverted
 5 siNA construct (Compound No. 31276/31279, Table III) and saline. Furthermore, ELISA analysis of VEGFr1 protein using the active siNA and inverted control siNA above showed significant reduction in the level of VEGFr1 protein expression using the active siNA compared to the inactive siNA construct. These results demonstrate that
 10 siNA molecules having different chemically modified compositions, such as the modifications described herein, are capable of significantly inhibiting neovascularization as shown in this model of intraocular administration.

Periocular Administration of siNA

Female C57BL/6 mice (4-5 weeks old) were anesthetized with a 0.2 ml of a mixture of ketamine/xylazine (8:1), and the pupils were dilated with a single drop of 1%
 15 tropicamide. Then a 532nm diode laser photocoagulation (75 μ m spot size, 0.1-s duration, 120 mW) was used to generate three laser spots in each eye surrounding the optic nerve by using a hand-held coverslip as a contact lens. A bubble formed at the laser spot indicating a rupture of the Bruch's membrane. Next, the laser spots were evaluated for the presence of CNV on day 17 after laser treatment.

20 After laser induction of multiple CNV lesions in mice, the siNA was administered via periocular injections under a dissecting microscope. Periocular injections were performed with a Harvard pump microinjection apparatus and pulled glass micropipets. Each micropipet was calibrated to deliver 5 μ L of vehicle containing test siNA at concentrations of 0.5 ug or 1.5 ug of siNA. The mice were anesthetized,
 25 pupils were dilated, and, the sharpened tip of the micropipet was passed, and the foot switch was depressed. Periocular injections were given daily starting at day 1 through day 14 after laser photocoagulation.

At the time of death, mice were anesthetized (ketamine/xylazine mixture, 8:1) and perfused through the heart with 1 mL PBS containing 50 mg/mL fluorescein-labeled dextran (FITC-Dextran, 2 million average molecular weight, Sigma). The eyes were
 30 removed and fixed overnight in 1% phosphate-buffered 4% Formalin. The cornea and

the lens were removed and the neurosensory retina was carefully dissected from the eyecup. Five radial cuts were made from the edge of the eyecup to the equator; the sclera-choroid-retinal pigment epithelium (RPE) complex was flat-mounted, with the sclera facing down, on a glass slide in Aquamount. Flat mounts were examined with a

5 Nikon fluorescence microscope. A laser spot with green vessels was scored CNV-positive, and a laser spot lacking green vessels was scored CNV-negative. Flatmounts were examined by fluorescence microscopy (Axioskop; Carl Zeiss, Thornwood, NY) and images were digitized with a three-color charge-coupled device (CCD) video camera and a frame grabber. Image-analysis software (Image-Pro Plus; Media Cybernetics, Silver

10 Spring, MD) was used to measure the total area of hyperfluorescence associated with each burn, corresponding to the total fibrovascular scar. The areas within each eye were averaged to give one experimental value per eye.

VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273, Table III) was tested for inhibition of VEGF-induced neovascularization at

15 two different concentrations (1.5 ug, and 0.5 ug dose response) as compared to a matched chemistry saline control and 0.5 ug inverted control siRNA construct (Compound No. 31276/31279, Table III). As shown in **Figure 18**, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is effective in inhibiting VEGFr1 induced neovascularization (20% inhibition) in the C57BL/6 mice

20 periocular delivery model compared to the matched chemistry inverted control siNA. The active siNA construct was also highly effective in inhibiting VEGFr1 induced neovascularization (54% inhibition) compared to the saline control. In an additional assay shown in **Figure 19**, VEGFr1 site 349 active siNA having “Stab 9/10” chemistry (Compound No. 31270/31273) at two concentrations was effective at inhibiting

25 neovascularization in CNV lesions compared to the inverted siNA control and the saline control. As shown in **Figure 19**, the active siNA construct having “Stab 9/10” chemistry (Compound No. 31270/31273) is effective in inhibiting VEGFr1 induced neovascularization (43% inhibition) in the C57BL/6 mice periocular delivery model compared to the matched chemistry inverted control siNA. The active siNA construct

30 was also effective in inhibiting VEGFr1 induced neovascularization (33% inhibition) compared to the saline control. These results demonstrate that siNA molecules having different chemically modified compositions, such as the modifications described herein,

are capable of significantly inhibiting neovascularization as shown in this model of periocular administration.

Example 11: Indications

The present body of knowledge in VEGF and/or VEGFr research indicates the need for methods to assay VEGF and/or VEGFr activity and for compounds that can regulate VEGF and/or VEGFr expression for research, diagnostic, and therapeutic use. As described herein, the nucleic acid molecules of the present invention can be used in assays to diagnose disease state related of VEGF and/or VEGFr levels. In addition, the nucleic acid molecules can be used to treat disease state related to VEGF and/or VEGFr levels.

Particular conditions and disease states that can be associated with VEGF and/or VEGFr expression modulation include, but are not limited to:

1) Tumor angiogenesis: Angiogenesis has been shown to be necessary for tumors to grow into pathological size (Folkman, 1971, *PNAS* 76, 5217-5221; Wellstein & Czubayko, 1996, *Breast Cancer Res and Treatment* 38, 109-119). In addition, it allows tumor cells to travel through the circulatory system during metastasis. Increased levels of gene expression of a number of angiogenic factors such as vascular endothelial growth factor (VEGF) have been reported in vascularized and edema-associated brain tumors (Berkman *et al.*, 1993 *J. Clin. Invest.* 91, 153). A more direct demonstration of the role of VEGF in tumor angiogenesis was demonstrated by Jim Kim *et al.*, 1993 *Nature* 362,841 wherein, monoclonal antibodies against VEGF were successfully used to inhibit the growth of rhabdomyosarcoma, glioblastoma multiforme cells in nude mice. Similarly, expression of a dominant negative mutated form of the flt-1 VEGF receptor inhibits vascularization induced by human glioblastoma cells in nude mice (Millauer *et al.*, 1994, *Nature* 367, 576). Specific tumor/cancer types that can be targeted using the nucleic acid molecules of the invention include but are not limited to the tumor/cancer types described herein.

2) Ocular diseases: Neovascularization has been shown to cause or exacerbate ocular diseases including, but not limited to, macular degeneration, neovascular glaucoma, diabetic retinopathy, myopic degeneration, and trachoma (Norrby, 1997,

APMIS 105, 417-437). Aiello *et al.*, 1994 *New Engl. J. Med.* 331, 1480, showed that the ocular fluid of a majority of patients suffering from diabetic retinopathy and other retinal disorders contains a high concentration of VEGF. Miller *et al.*, 1994 *Am. J. Pathol.* 145, 574, reported elevated levels of VEGF mRNA in patients suffering from retinal ischemia. These observations support a direct role for VEGF in ocular diseases. Other factors, including those that stimulate VEGF synthesis, may also contribute to these indications.

3) Dermatological Disorders: Many indications have been identified which may be angiogenesis dependent, including but not limited to, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, and Osler-Weber-Rendu syndrome (Norrby, *supra*). Intradermal injection of the angiogenic factor b-FGF demonstrated angiogenesis in nude mice (Weckbecker *et al.*, 1992, *Angiogenesis: Key principles-Science-Technology-Medicine*, ed R. Steiner). Detmar *et al.*, 1994 *J. Exp. Med.* 180, 1141 reported that VEGF and its receptors were over-expressed in psoriatic skin and psoriatic dermal microvessels, suggesting that VEGF plays a significant role in psoriasis.

4) Rheumatoid arthritis: Immunohistochemistry and *in situ* hybridization studies on tissues from the joints of patients suffering from rheumatoid arthritis show an increased level of VEGF and its receptors (Fava *et al.*, 1994 *J. Exp. Med.* 180, 341). Additionally, Koch *et al.*, 1994 *J. Immunol.* 152, 4149, found that VEGF-specific antibodies were able to significantly reduce the mitogenic activity of synovial tissues from patients suffering from rheumatoid arthritis. These observations support a direct role for VEGF in rheumatoid arthritis. Other angiogenic factors including those of the present invention may also be involved in arthritis.

5) Endometriosis: Various studies indicate that VEGF is directly implicated in endometriosis. In one study, VEGF concentrations measured by ELISA in peritoneal fluid were found to be significantly higher in women with endometriosis than in women without endometriosis (24.1 ± 15 ng/ml vs 13.3 ± 7.2 ng/ml in normals). In patients with endometriosis, higher concentrations of VEGF were detected in the proliferative phase of the menstrual cycle (33 ± 13 ng/ml) compared to the secretory phase (10.7 ± 5 ng/ml). The cyclic variation was not noted in fluid from normal patients (McLaren *et al.*, 1996,

Human Reprod. 11, 220-223). In another study, women with moderate to severe endometriosis had significantly higher concentrations of peritoneal fluid VEGF than women without endometriosis. There was a positive correlation between the severity of endometriosis and the concentration of VEGF in peritoneal fluid. In human endometrial biopsies, VEGF expression increased relative to the early proliferative phase approximately 1.6-, 2-, and 3.6-fold in midproliferative, late proliferative, and secretory endometrium (Shifren *et al.*, 1996, *J. Clin. Endocrinol. Metab.* 81, 3112-3118). In a third study, VEGF-positive staining of human ectopic endometrium was shown to be localized to macrophages (double immunofluorescent staining with CD14 marker). Peritoneal fluid macrophages demonstrated VEGF staining in women with and without endometriosis. However, increased activation of macrophages (acid phosphatase activity) was demonstrated in fluid from women with endometriosis compared with controls. Peritoneal fluid macrophage conditioned media from patients with endometriosis resulted in significantly increased cell proliferation ($[^3\text{H}]$ thymidine incorporation) in HUVEC cells compared to controls. The percentage of peritoneal fluid macrophages with VEGFr2 mRNA was higher during the secretory phase, and significantly higher in fluid from women with endometriosis ($80 \pm 15\%$) compared with controls ($32 \pm 20\%$). Flt-mRNA was detected in peritoneal fluid macrophages from women with and without endometriosis, but there was no difference between the groups or any evidence of cyclic dependence (McLaren *et al.*, 1996, *J. Clin. Invest.* 98, 482-489). In the early proliferative phase of the menstrual cycle, VEGF has been found to be expressed in secretory columnar epithelium (estrogen-responsive) lining both the oviducts and the uterus in female mice. During the secretory phase, VEGF expression was shown to have shifted to the underlying stroma composing the functional endometrium. In addition to examining the endometrium, neovascularization of ovarian follicles and the corpus luteum, as well as angiogenesis in embryonic implantation sites have been analyzed. For these processes, VEGF was expressed in spatial and temporal proximity to forming vasculature (Shweiki *et al.*, 1993, *J. Clin. Invest.* 91, 2235-2243).

6) Kidney disease: Autosomal dominant polycystic kidney disease (ADPKD) is the most common life threatening hereditary disease in the USA. It affects about 1:400 to 1:1000 people and approximately 50% of people with ADPKD develop renal failure. ADPKD accounts for about 5-10% of end-stage renal failure in the USA, requiring

dialysis and renal transplantation. Angiogenesis is implicated in the progression of ADPKD for growth of cyst cells, as well as increased vascular permeability promoting fluid secretion into cysts. Proliferation of cystic epithelium is a feature of ADPKD because cyst cells in culture produce soluble vascular endothelial growth factor (VEGF).

5 VEGFr1 has been detected in epithelial cells of cystic tubules but not in endothelial cells in the vasculature of cystic kidneys or normal kidneys. VEGFr2 expression is increased in endothelial cells of cyst vessels and in endothelial cells during renal ischemia-reperfusion.

The use of radiation treatments and chemotherapeutics, such as Gemcytabine and
 10 cyclophosphamide, are non-limiting examples of chemotherapeutic agents that can be combined with or used in conjunction with the nucleic acid molecules (*e.g.* siNA molecules) of the instant invention. Those skilled in the art will recognize that other anti-cancer compounds and therapies can similarly be readily combined with the nucleic acid molecules of the instant invention (*e.g.* siNA molecules) and are hence within the
 15 scope of the instant invention. Such compounds and therapies are well known in the art (see for example *Cancer: Principles and Practice of Oncology*, Volumes 1 and 2, eds Devita, V.T., Hellman, S., and Rosenberg, S.A., J.B. Lippincott Company, Philadelphia, USA; incorporated herein by reference) and include, without limitation, folates, antifolates, pyrimidine analogs, fluoropyrimidines, purine analogs, adenosine analogs,
 20 topoisomerase I inhibitors, anthracyclins, platinum analogs, alkylating agents, nitrosoureas, plant derived compounds such as vinca alkaloids, epipodophyllotoxins, tyrosine kinase inhibitors, taxols, radiation therapy, surgery, nutritional supplements, gene therapy, radiotherapy, for example 3D-CRT, immunotoxin therapy, for example ricin, and monoclonal antibodies. Specific examples
 25 of chemotherapeutic compounds that can be combined with or used in conjunction with the nucleic acid molecules of the invention include, but are not limited to, Paclitaxel; Docetaxel; Methotrexate; Doxorubin; Edatrexate; Vinorelbine; Tomaxifen; Leucovorin; 5-fluoro uridine (5-FU); Irotectan; Cisplatin; Carboplatin; Amsacrine; Cytarabine; Bleomycin; Mitomycin C; Dactinomycin; Mithramycin; Hexamethylmelamine;
 30 Dacarbazine; L-asparaginase; Nitrogen mustard; Melphalan, Chlorambucil; Busulfan; Ifosfamide; 4-hydroperoxycyclophosphamide; Thiotepa; Irinotecan (CAMPTOSAR®, CPT-11, Camptothecin-11, Campto) Tamoxifen; Herceptin; IMC C225; ABX-EGF; and

combinations thereof. The above list of compounds are non-limiting examples of compounds and/or methods that can be combined with or used in conjunction with the nucleic acid molecules (e.g. siNA) of the instant invention. Those skilled in the art will recognize that other drug compounds and therapies can similarly be readily combined with the nucleic acid molecules of the instant invention (e.g., siNA molecules) are hence
5 within the scope of the instant invention.

Example 12: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of
10 applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or
15 exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as
20 well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g.,
25 multiple siNA molecules targeted to different genes, siNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such
30 RNA is detected by determining the presence of a cleavage product after treatment with a siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms of target RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches
5 one skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting
10 and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically
15 disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and
20 described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be
25 within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Table I: VEGF and VEGFr Accession Numbers

5	NM_005429 Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA gi 19924300 ref NM_005429.2 [19924300]
10	NM_003376 Homo sapiens vascular endothelial growth factor (VEGF), mRNA gi 19923239 ref NM_003376.2 [19923239]
15	AF095785 Homo sapiens vascular endothelial growth factor (VEGF) gene, promoter region and partial cds
20	gi 4154290 gb AF095785.1 [4154290]
25	NM_003377 Homo sapiens vascular endothelial growth factor B (VEGFB), mRNA gi 20070172 ref NM_003377.2 [20070172]
30	AF486837 Homo sapiens vascular endothelial growth factor isoform VEGF165 (VEGF) mRNA, complete cds
35	gi 19909064 gb AF486837.1 [19909064]
40	AF468110 Homo sapiens vascular endothelial growth factor B isoform (VEGFB) gene, complete cds, alternatively spliced
	gi 18766397 gb AF468110.1 [18766397]
45	AF437895 Homo sapiens vascular endothelial growth factor (VEGF) gene, partial cds gi 16660685 gb AF437895.1 AF437895[16660685]
50	AY047581

Homo sapiens vascular endothelial growth factor (VEGF)
mRNA, complete cds
gi|15422108|gb|AY047581.1|[15422108]

5
AF063657
Homo sapiens vascular endothelial growth factor
receptor (FLT1) mRNA, complete
cds
10 gi|3132830|gb|AF063657.1|AF063657[3132830]

AF092127
Homo sapiens vascular endothelial growth factor (VEGF)
15 gene, partial sequence
gi|4139168|gb|AF092127.1|AF092127[4139168]

AF092126
20 Homo sapiens vascular endothelial growth factor (VEGF)
gene, 5' UTR
gi|4139167|gb|AF092126.1|AF092126[4139167]

25 AF092125
Homo sapiens vascular endothelial growth factor (VEGF)
gene, partial cds
gi|4139165|gb|AF092125.1|AF092125[4139165]

30 E15157
Human VEGF mRNA
gi|5709840|dbj|E15157.1||pat|JP|1998052285|2[5709840]

35 E15156
Human VEGF mRNA
gi|5709839|dbj|E15156.1||pat|JP|1998052285|1[5709839]

40 E14233
Human mRNA for vascular endothelial growth factor
(VEGF), complete cds
gi|5708916|dbj|E14233.1||pat|JP|1997286795|1[5708916]

45 AF024710
Homo sapiens vascular endothelial growth factor (VEGF)
mRNA, 3'UTR
50 gi|2565322|gb|AF024710.1|AF024710[2565322]

5 AJ010438
 Homo sapiens mRNA for vascular endothelial growth
 factor, splicing variant
 VEGF183
 gi|3647280|emb|AJ010438.1|HSA010438[3647280]

10 AF098331
 Homo sapiens vascular endothelial growth factor (VEGF)
 gene, promoter, partial
 sequence
 gi|4235431|gb|AF098331.1|AF098331[4235431]

15
 AF022375
 Homo sapiens vascular endothelial growth factor mRNA,
 complete cds
 20 gi|3719220|gb|AF022375.1|AF022375[3719220]

AH006909
 vascular endothelial growth factor {alternative
 25 splicing} [human, Genomic, 414
 nt 5 segments]
 gi|1680143|gb|AH006909.1||bbm|191843[1680143]

30 U01134
 Human soluble vascular endothelial cell growth factor
 receptor (sflt) mRNA,
 complete cds
 35 gi|451321|gb|U01134.1|U01134[451321]

E14000
 Human mRNA for FLT
 40 gi|3252767|dbj|E14000.1||pat|JP|1997255700|1[3252767]

E13332
 cDNA encoding vascular endodermal cell growth factor
 VEGF
 45 gi|3252137|dbj|E13332.1||pat|JP|1997173075|1[3252137]

E13256
 Human mRNA for FLT, complete cds
 50 gi|3252061|dbj|E13256.1||pat|JP|1997154588|1[3252061]

5 AF063658
 Homo sapiens vascular endothelial growth factor
 receptor 2 (KDR) mRNA, complete
 cds
 gi|3132832|gb|AF063658.1|AF063658[3132832]

10 AJ000185
 Homo Sapiens mRNA for vascular endothelial growth
 factor-D
 gi|2879833|emb|AJ000185.1|HSAJ185[2879833]

15 D89630
 Homo sapiens mRNA for VEGF-D, complete cds
 gi|2780339|dbj|D89630.1|[2780339]

20 AF035121
 Homo sapiens KDR/flk-1 protein mRNA, complete cds
 gi|2655411|gb|AF035121.1|AF035121[2655411]

25 AF020393
 Homo sapiens vascular endothelial growth factor C
 gene, partial cds and 5'
 upstream region
 gi|2582366|gb|AF020393.1|AF020393[2582366]

30
 Y08736
 H.sapiens vegf gene, 3'UTR
 gi|1619596|emb|Y08736.1|HSVEGF3UT[1619596]

35
 X62568
 H.sapiens vegf gene for vascular endothelial growth
 factor
 gi|37658|emb|X62568.1|HSVEGF[37658]

40
 X94216
 H.sapiens mRNA for VEGF-C protein
 gi|1177488|emb|X94216.1|HSVEGFC[1177488]

45
 NM_002020
 Homo sapiens fms-related tyrosine kinase 4 (FLT4),
 mRNA
 gi|4503752|ref|NM_002020.1|[4503752]

50

5 NM_002253
Homo sapiens kinase insert domain receptor (a type III
receptor tyrosine kinase)
(KDR), mRNA
gi|11321596|ref|NM_002253.1|[11321596]

Table II: VEGFr siNA and Target Sequences

Pos	Target Sequence	Seq ID	UPos	Upper seq	Seq ID	LPos	Lower seq	Seq ID
1	GCGGACACUCUCUGGCU	1	1	GCGGACACUCUCUGGCU	1	23	AGCCGAGGAGGAGUCCGC	428
19	UCCUCCCCGAGCGGCGG	2	19	UCCUCCCCGAGCGGCGG	2	41	CCGCCGUCUGCCGGGAGGA	429
37	GCGGUCGGAGCGGGCUCC	3	37	GCGGUCGGAGCGGGCUCC	3	59	GGAGCCCGCUCGAGCCGC	430
55	GCGGUCUGGGUGCAGCGG	4	55	GCGGUCUGGGUGCAGCGG	4	77	CCGUCGACCCGAGCCCGC	431
73	GCCAGCGGGCCUGGCGCG	5	73	GCCAGCGGGCCUGGCGCG	5	95	CGCCGCCAGGCCCGCUGGC	432
91	GAGGAUACCCGGGGAAGU	6	91	GAGGAUACCCGGGGAAGU	6	113	ACUUCGCCGGGUAUCCUC	433
109	UGGUUGUCUCUGGCUUGA	7	109	UGGUUGUCUCUGGCUUGA	7	131	UCCAGCCAGGAGACAACCA	434
127	AGCCGCGAGACGGGCGCUC	8	127	AGCCGCGAGACGGGCGCUC	8	149	GAGCGCCCGUCUCGCGGCU	435
145	CAGGCGCGGGCCGCGCGG	9	145	CAGGCGCGGGCCGCGCGG	9	167	CCGCCGGCCCCGCGCCUC	436
163	GCGGCGAACGAGAGACGG	10	163	GCGGCGAACGAGAGACGG	10	185	CCGUCCUCUCGUUCGCGCG	437
181	GACUCUGCGGCGCGGUCG	11	181	GACUCUGCGGCGCGGUCG	11	203	CGACCCGGCCCGCAGAGUC	438
199	GUUGCGCGGGAGCGCGG	12	199	GUUGCGCGGGAGCGCGG	12	221	CCGCGUCUCCCCGGCCAAC	439
217	GGACCGGGCGAGCAGGCC	13	217	GGACCGGGCGAGCAGGCC	13	239	GGCCUGCUCGCCCGGUGCC	440
235	CGCGUCGCGCUCACCAUGG	14	235	CGCGUCGCGCUCACCAUGG	14	257	CCAUGGUGAGCGCGACGCG	441
253	GUCAGCUACUGGACACCG	15	253	GUCAGCUACUGGACACCG	15	275	CGGUGUCCAGUAGCUGAC	442
271	GGGUCCUGCUGUGCGCGC	16	271	GGGUCCUGCUGUGCGCGC	16	293	GCGCGACAGCAGGACCCC	443
289	CUGCUCAGCUCUCUGCUUC	17	289	CUGCUCAGCUCUCUGCUUC	17	311	GAAGCAGACAGCUGAGCAG	444
307	CUCACAGGAUCUAGUUCAG	18	307	CUCACAGGAUCUAGUUCAG	18	329	CUGAACUAGAUCUUGAG	445
325	GGUUCAAAAUUAAAAGAU	19	325	GGUUCAAAAUUAAAAGAU	19	347	GAUCUUUUUUUUUGAAC	446
343	CCUGAACUGAGUUUAAAAG	20	343	CCUGAACUGAGUUUAAAAG	20	365	CUUUUAAACUCAGUUCAGG	447
361	GGACCCAGCACAUCAUUC	21	361	GGACCCAGCACAUCAUUC	21	383	GCAUGAUGUCUGGUGGCC	448
379	CAAGCAGGCCAGACACUGC	22	379	CAAGCAGGCCAGACACUGC	22	401	GCAGUGUCUGGCCUGCUUG	449
397	CAUCUCCAUGCAGGGGGG	23	397	CAUCUCCAUGCAGGGGGG	23	419	CCCCCUGCAUUGGAGAU	450
415	GAAGCAGCCCAUAAAUGGU	24	415	GAAGCAGCCCAUAAAUGGU	24	437	ACCAUUUUAUGGGCUGCUUC	451
433	UCUUUGCCUGAAAUGGUGA	25	433	UCUUUGCCUGAAAUGGUGA	25	455	UCACCAUUUUCAGGCAAGA	452
451	AGUAAGGAAAGCGAAAGGC	26	451	AGUAAGGAAAGCGAAAGGC	26	473	GCCUUUCGUUUCUUUACU	453
469	CUGAGCAUAACUAAAUCUG	27	469	CUGAGCAUAACUAAAUCUG	27	491	CAGAUUUUAGUUUAGCUCAG	454
487	GCCUGUGGAAGAAAUGGCA	28	487	GCCUGUGGAAGAAAUGGCA	28	509	UGCCAUUUUCUCCACAGGC	455
505	AAACAAUUCUGCAGUACUU	29	505	AAACAAUUCUGCAGUACUU	29	527	AAGUACUGCAGAAUUGUUU	456
523	UUAACCUUGAACACAGCUC	30	523	UUAACCUUGAACACAGCUC	30	545	GAGCUGUGUUUAAGGUUAA	457

541	CAAGCAAAACACACUGGCU	31	541	CAAGCAAAACACACUGGCU	31	563	AGCCAGUGUGUUUGCUUG	458
559	UUCUACAGCUGCAAAUAUC	32	559	UUCUACAGCUGCAAAUAUC	32	581	GAUUAUUUGCAGCUGUAGAA	459
577	CUAGCUGUACCUACUUA	33	577	CUAGCUGUACCUACUUA	33	599	UUGAAGUAGGUACAGCUAG	460
595	AAGAAGAAGAAACAGAAU	34	595	AAGAAGAAGAAACAGAAU	34	617	AUUCUGUUUCCUUCUUCUU	461
613	UCUGCAAUCUAUAUUUA	35	613	UCUGCAAUCUAUAUUUA	35	635	UAAUAUAUAGAUUGCAGA	462
631	AUUAGUGAUACAGGUAGAC	36	631	AUUAGUGAUACAGGUAGAC	36	653	GUCUACCCUGUAUCACUAAU	463
649	CCUUUCGUAAGAGUUA	37	649	CCUUUCGUAAGAGUUA	37	671	UGUACAUUCUACGAAAGG	464
667	AGUAAAUCGCGAAUUA	38	667	AGUAAAUCGCGAAUUA	38	689	UAAUUUCGGGAUUUUCACU	465
685	AUACACAUACUGAAGGAA	39	685	AUACACAUACUGAAGGAA	39	707	UUCUUUCAGUCAUGUGUUA	466
703	AGGAGCUCGUAUUCUU	40	703	AGGAGCUCGUAUUCUU	40	725	AGGAAUGACGAGCUCUU	467
721	UGCCGGGUACGUCACCUA	41	721	UGCCGGGUACGUCACCUA	41	743	UAGGUGACGUAAACCCGGA	468
739	AACAUACAGUUACUUUA	42	739	AACAUACAGUUACUUUA	42	761	UUAAGUAACAGUGUGUU	469
757	AAAAAGUUUCCACUUUGACA	43	757	AAAAAGUUUCCACUUUGACA	43	779	UGUCAAGUGGAAACUUUUU	470
775	ACUUUGAUUCCUGAUGGAA	44	775	ACUUUGAUUCCUGAUGGAA	44	797	UCCAUACAGGGAUCAAAGU	471
793	AAACGCAUAUUCUGGACA	45	793	AAACGCAUAUUCUGGACA	45	815	UGUCCAUAGUUUUGCUUU	472
811	AGUAGAAAGGGCUUAUCA	46	811	AGUAGAAAGGGCUUAUCA	46	833	UGUAAGGCCUUUCUACU	473
829	AUAUCAAUUGCAACGUACA	47	829	AUAUCAAUUGCAACGUACA	47	851	UGUACGUUGCAUUUGUAU	474
847	AAAGAAUAGGGCUUCUGA	48	847	AAAGAAUAGGGCUUCUGA	48	869	UCAGAAAGCCUUAUUUCUU	475
865	ACUGUGAAAGCAACAGUCA	49	865	ACUGUGAAAGCAACAGUCA	49	887	UGACUGUUUGCUUACACAGU	476
883	AUUGGGCAUUUGUAUAGA	50	883	AUUGGGCAUUUGUAUAGA	50	905	UCUUAUACAAUUGCCCAUU	477
901	ACAAACUAUCACACAUUC	51	901	ACAAACUAUCACACAUUC	51	923	GAUGUGUGAGAUAGUUUGU	478
919	CGACAAACCAUUAUACA	52	919	CGACAAACCAUUAUACA	52	941	UGAUUGUAUUUGGUUUGUG	479
937	AUAGAUUGCCAAUAAGCA	53	937	AUAGAUUGCCAAUAAGCA	53	959	UGCUUAUUUGGACAUUCUAU	480
955	ACACCACGCCAGUCAAU	54	955	ACACCACGCCAGUCAAU	54	977	AUUUGACUGGGCGUGGUGU	481
973	UUACUUAGAGGCCAUACUC	55	973	UUACUUAGAGGCCAUACUC	55	995	GAGUAUUGGCCUCUAAAGUAA	482
991	CUUGUCCUAUUUGUACUG	56	991	CUUGUCCUAUUUGUACUG	56	1013	CAGUACAAUUGAGGACAAG	483
1009	GUUACCAUCCUUUGAACA	57	1009	GUUACCAUCCUUUGAACA	57	1031	UGUUAAGGGGAGUGGUAGC	484
1027	ACGAGAUUCAAUUGACCU	58	1027	ACGAGAUUCAAUUGACCU	58	1049	AGGUCAUUUGAACUCUCUGU	485
1045	UGGAGUUACCCUGAUGAAA	59	1045	UGGAGUUACCCUGAUGAAA	59	1067	UUUCAUCAGGGUAACUCCA	486
1063	AAAAUUAAGAGAGCUUCCG	60	1063	AAAAUUAAGAGAGCUUCCG	60	1085	CGGAAGCUCUCUUAUUUUU	487
1081	GUUAGGCGACGAAUUGACC	61	1081	GUUAGGCGACGAAUUGACC	61	1103	GGUCAAUUCGUCGCCUJAC	488
1099	CAAGCAUUUCCCAUGCCA	62	1099	CAAGCAUUUCCCAUGCCA	62	1121	UGGCAUUGGGAUUUGCUUUG	489
1117	AACAUUUUCUACAGUGUUC	63	1117	AACAUUUUCUACAGUGUUC	63	1139	GAACACUGUAGAAUUGUU	490
1135	CUUACUAUUUGACAAAAUUC	64	1135	CUUACUAUUUGACAAAAUUC	64	1157	GCAUUUUUGUCAUUAAG	491
1153	CAGAAACAAAGACAAAGGAC	65	1153	CAGAAACAAAGACAAAGGAC	65	1175	GUCCUUUGUCUUUGUUCUG	492
1171	CUUUUAUACUUGUCUGUUA	66	1171	CUUUUAUACUUGUCUGUUA	66	1193	UUACACGACAAAGUAUAAAG	493

1189	AGGAGUGGACCAUCAUUA	67	1189	AGGAGUGGACCAUCAUUA	67	1211	UGAAUGAUGGUCCACUCCU	494
1207	AAUCUGUUAAACACCUCAG	68	1207	AAUCUGUUAAACACCUCAG	68	1229	CUGAGGUGUUAAACAGAUUU	495
1225	GUGCAUAUAUAUGAUAAAG	69	1225	GUGCAUAUAUAUGAUAAAG	69	1247	CUUUAUCAUAUAUAUGCAC	496
1243	GCAUUAUCACUGUGAAAC	70	1243	GCAUUAUCACUGUGAAAC	70	1265	GUUUCACAGUGAUGAAUGC	497
1261	CAUCGAAACACGAGGUGC	71	1261	CAUCGAAACACGAGGUGC	71	1283	GCACCUGCUGUUUUCGAUG	498
1279	CUUGAAACCGUAGCUGGCA	72	1279	CUUGAAACCGUAGCUGGCA	72	1301	UGCCAGCUACGGUUUCAAAG	499
1297	AAGCGGUCUUACCGGCUCU	73	1297	AAGCGGUCUUACCGGCUCU	73	1319	AGAGCCGGUAAAGACC CGCUU	500
1315	UCUAUGAAAGUGAAGGCAU	74	1315	UCUAUGAAAGUGAAGGCAU	74	1337	AUGCCUUACAUUUAUAGA	501
1333	UUUCCUCGCGGGAAGUUG	75	1333	UUUCCUCGCGGGAAGUUG	75	1355	CAACUUCGCGGAGGGAAA	502
1351	GUUGGUUAAAAGAUUGGU	76	1351	GUUGGUUAAAAGAUUGGU	76	1373	ACCCAUUUUUAAACCAUAC	503
1369	UUACCUGCGACUGAGAAAU	77	1369	UUACCUGCGACUGAGAAAU	77	1391	AUUUCACAGUCGACGGUAA	504
1387	UCUGCUCGCUAUUUUGACUC	78	1387	UCUGCUCGCUAUUUUGACUC	78	1409	GAGUCAAUAGCGAGCAGA	505
1405	CGUGGCUACUCGUUAAUUA	79	1405	CGUGGCUACUCGUUAAUUA	79	1427	UAUUAAACGAGUAGCCACG	506
1423	AUCAAGGACGUAACUGAAG	80	1423	AUCAAGGACGUAACUGAAG	80	1445	UUUCAGUUACGUCCUUGAU	507
1441	GAGGAUGCAGGGAAUUAUA	81	1441	GAGGAUGCAGGGAAUUAUA	81	1463	UUUAUUCCCUAGUCCUUCU	508
1459	ACAAUCUUGCUGAGCAUAA	82	1459	ACAAUCUUGCUGAGCAUAA	82	1481	UUUAGCUCAGCAAGAUUGU	509
1477	AAACAGUCAAAUGUGUUUA	83	1477	AAACAGUCAAAUGUGUUUA	83	1499	UAAACACAUUUGACUGUUU	510
1495	AAAACUCACUGCCACUC	84	1495	AAAACUCACUGCCACUC	84	1517	GAGUGGACAGUGAGGUUUU	511
1513	CUAAUUGUCAUUGUGAAAC	85	1513	CUAAUUGUCAUUGUGAAAC	85	1535	GUUUCACAUUAGACAAUUAAG	512
1531	CCCAGAUUUACGAAAGG	86	1531	CCCAGAUUUACGAAAGG	86	1553	CCUUUUCGUAAAUUCUGGGG	513
1549	GCCGUGUCAUCGUUUCAG	87	1549	GCCGUGUCAUCGUUUCAG	87	1571	CUGGAAACGAGACACGGC	514
1567	GACCCGGCUCUACCCAC	88	1567	GACCCGGCUCUACCCAC	88	1589	GUGGUAAGAGAGCCCGGUC	515
1585	CUGGGCAGCAGACAAUCC	89	1585	CUGGGCAGCAGACAAUCC	89	1607	GGUUUUGUCUGCUGCCAG	516
1603	CUGACUUUACCGCAUAUG	90	1603	CUGACUUUACCGCAUAUG	90	1625	CAUAUGCGGUACAAGUCAG	517
1621	GGUAUCCCUCAACCUACAA	91	1621	GGUAUCCCUCAACCUACAA	91	1643	UUUAGGUUUGAGGGUAACC	518
1639	AUCAAGUGGUUUCUGGCACC	92	1639	AUCAAGUGGUUUCUGGCACC	92	1661	GGUGCCAGAACCCACUUGAU	519
1657	CCUGUAACCAUAUAUUAU	93	1657	CCUGUAACCAUAUAUUAU	93	1679	AAUGAUUAUGGUUACAGGG	520
1675	UCCGAAGCAAGGUGUGACU	94	1675	UCCGAAGCAAGGUGUGACU	94	1697	AGUCACACCUUGCUUCGGA	521
1693	UUUUGUCCAAUAUAUGAAG	95	1693	UUUUGUCCAAUAUAUGAAG	95	1715	CUUCAUAUUGGAACAAA	522
1711	GAGUCCUUUAUCCUGGAUG	96	1711	GAGUCCUUUAUCCUGGAUG	96	1733	CAUCCAGGAUAAAGGACUC	523
1729	GCUGACAGCAACAUUGGAA	97	1729	GCUGACAGCAACAUUGGAA	97	1751	UUCCCAUGUUGCUGACGC	524
1747	AACAGAAUUGAGAGCAUCA	98	1747	AACAGAAUUGAGAGCAUCA	98	1769	UGAUGCUCUCAAUUCUGUU	525
1765	ACUCAGCGCAUGGCAAUAA	99	1765	ACUCAGCGCAUGGCAAUAA	99	1787	UUUUUGCCAUUGCGCUGAGU	526
1783	AUAGAAGGAAAGAAUAAGA	100	1783	AUAGAAGGAAAGAAUAAGA	100	1805	UCUUUAUUUUUCCUUCUUAU	527
1801	AUGGCUAGCACCUUGGUUG	101	1801	AUGGCUAGCACCUUGGUUG	101	1823	CAACCAAGGUGCUAGCCAU	528
1819	GUGGCUGACUCUAGAAUUU	102	1819	GUGGCUGACUCUAGAAUUU	102	1841	AAAUUCUAGAGUCAGCCAC	529

1837	UCUGGAAUUCUACAUUUUGCA	103	1837	UCUGGAAUUCUACAUUUUGCA	103	1859	UGCAAAUUGUAGAUUCCAGA	530
1855	AUAGCUUCCAAUAAAGUUG	104	1855	AUAGCUUCCAAUAAAGUUG	104	1877	CAACUUUUUUUGGAAAGCUAU	531
1873	GGGACUGUGGGAAGAAACA	105	1873	GGGACUGUGGGAAGAAACA	105	1895	UGUUUCUUCGCCACAGUCCC	532
1891	AUAGCUUUUUUAUACACAG	106	1891	AUAGCUUUUUUAUACACAG	106	1913	CUGUGAUUAAUAAAGCUUUAU	533
1909	GAUGUGCCAAUUGGUUUC	107	1909	GAUGUGCCAAUUGGUUUC	107	1931	GAACCCCAUUUGGCACAUC	534
1927	CAUGUUAAUUGGAAAAA	108	1927	CAUGUUAAUUGGAAAAA	108	1949	UUUUUCCAAAGUUAAACAUG	535
1945	AUGCCGACGGAAGGAGAGG	109	1945	AUGCCGACGGAAGGAGAGG	109	1967	CCUCUCUUCGCGGCGCAU	536
1963	GACCGAAACUGUCUUGCA	110	1963	GACCGAAACUGUCUUGCA	110	1985	UGCAAGACAGUUUCAGGUC	537
1981	ACAGUUAAACAAGUUCUUAU	111	1981	ACAGUUAAACAAGUUCUUAU	111	2003	AUAAGAACUUUGUUAAACUGU	538
1999	UACAGAGACGUUACUUGGA	112	1999	UACAGAGACGUUACUUGGA	112	2021	UCCAAGUAACGUCUCUGUA	539
2017	AUUUACUGCGGACAGUUA	113	2017	AUUUACUGCGGACAGUUA	113	2039	UACUGUCCCGCAGUAAAAU	540
2035	AAUAAACAGAACAAUGCACU	114	2035	AAUAAACAGAACAAUGCACU	114	2057	AGUGCAUUUGUUCUGUUAUU	541
2053	UACAGUAAUAGCAAGCAAA	115	2053	UACAGUAAUAGCAAGCAAA	115	2075	UUUGCUUUGCUAAUACUGUA	542
2071	AAAAUGGCCAUACACUAAAGG	116	2071	AAAAUGGCCAUACACUAAAGG	116	2093	CCUUAGUGAUGGCCAUUUU	543
2089	GAGCACUCCAUACACUCUUA	117	2089	GAGCACUCCAUACACUCUUA	117	2111	UAAGAGUGAUGGAGUGCUC	544
2107	AAUCUUACCAUCAUGAAUG	118	2107	AAUCUUACCAUCAUGAAUG	118	2129	CAUUAGCAUGGUAAGAAU	545
2125	GUUUCCUGCAAGAUUCAG	119	2125	GUUUCCUGCAAGAUUCAG	119	2147	CUGAAUCUUGCAGGAAAC	546
2143	GGCACCUAUGCCUGCAGAG	120	2143	GGCACCUAUGCCUGCAGAG	120	2165	CUCUGCAGGCAUAGGUGCC	547
2161	GGCAGGAUUGUAUACACAG	121	2161	GGCAGGAUUGUAUACACAG	121	2183	CUGUGUAUACAUUCCUGGC	548
2179	GGGGAAGAAUCCUCCAGA	122	2179	GGGGAAGAAUCCUCCAGA	122	2201	UCUGGAGGAUUUCUCCCC	549
2197	AAGAAAGAAUUACAAUCA	123	2197	AAGAAAGAAUUACAAUCA	123	2219	UGAUUGAAUUUCUUCUUU	550
2215	AGAGAUACAGGAAGCACCAU	124	2215	AGAGAUACAGGAAGCACCAU	124	2237	AUGGUGCUUCCUGAUCUCU	551
2233	UACCUCCUGCGAAACCUCA	125	2233	UACCUCCUGCGAAACCUCA	125	2255	UGAGGUUUUCGACAGGAGUA	552
2251	AGUGAUCACACAGUGGCCA	126	2251	AGUGAUCACACAGUGGCCA	126	2273	UGGCCACUGUGUGAUCACU	553
2269	AUCAGCAGUUCACCCACU	127	2269	AUCAGCAGUUCACCCACU	127	2291	AAGUGGUGGAACUCUGCAU	554
2287	UUAGACUGUCAUGCUAAUG	128	2287	UUAGACUGUCAUGCUAAUG	128	2309	CAUUAGCAUGACAGUCUAA	555
2305	GGUGUCCCCGAGCCUCAGA	129	2305	GGUGUCCCCGAGCCUCAGA	129	2327	UCUGAGGCUCGGGACACC	556
2323	AUCACUUUGGUUUAAAAACA	130	2323	AUCACUUUGGUUUAAAAACA	130	2345	UGUUUUUAAACCAAGUGAU	557
2341	AACCAAAAAUACAACAAG	131	2341	AACCAAAAAUACAACAAG	131	2363	CUUGUUUGAUUUUUGGUU	558
2359	GAGCCUGGAAUUUUUUUAG	132	2359	GAGCCUGGAAUUUUUUUAG	132	2381	CUAAAAUAAUCCAGGCUC	559
2377	GGACCAGGAAGCAGCACGC	133	2377	GGACCAGGAAGCAGCACGC	133	2399	GCUGCUGCUUCCUGGUCC	560
2395	CUGUUUUUUGAAAGAGUCA	134	2395	CUGUUUUUUGAAAGAGUCA	134	2417	UGACUCUUUCAAUAAACAG	561
2413	ACAGAAGAGGAUAAAGGUG	135	2413	ACAGAAGAGGAUAAAGGUG	135	2435	CACCUUACUCCUCUUCUGU	562
2431	GUCUAUCACUGCAAAAGCCA	136	2431	GUCUAUCACUGCAAAAGCCA	136	2453	UGGCUUUUGCAGUGAUAGAC	563
2449	ACCAACCAGAAAGGCUCUG	137	2449	ACCAACCAGAAAGGCUCUG	137	2471	CAGAGCCCUUCUGGUUGGU	564
2467	GUGGAAAGUUACGCAUACC	138	2467	GUGGAAAGUUACGCAUACC	138	2489	GGUAUGCUGAAACUUUCCAC	565

2485	CUCACUGUUAAGGAACCU	139	2485	CUCACUGUUAAGGAACCU	139	2507	AGGUUCCUUGAACAGUGAG	566
2503	UCGGACAAGUCUAAUCUGG	140	2503	UCGGACAAGUCUAAUCUGG	140	2525	CCAGAUUAGACUUGUCCGA	567
2521	GAGCUGAUCACUCUAACAU	141	2521	GAGCUGAUCACUCUAACAU	141	2543	AUGUAGAGUGAUCAGCUC	568
2539	UGCACCUGUGGCGUGCGA	142	2539	UGCACCUGUGGCGUGCGA	142	2561	UCGCAGCCACACAGGUGCA	569
2557	ACUCUCUUCUGGCUCCUUA	143	2557	ACUCUCUUCUGGCUCCUUA	143	2579	AUAGGAGCCAGAAAGAGAGU	570
2575	UUAACCCUCCUUAUCCGAA	144	2575	UUAACCCUCCUUAUCCGAA	144	2597	UUCGGAUAAAGGAGGUAUA	571
2593	AAAUGAAAAGGUCUUCUU	145	2593	AAAUGAAAAGGUCUUCUU	145	2615	AAGAAGACCUUUUUAUUAUU	572
2611	UCUGAAUAAAGACUGACU	146	2611	UCUGAAUAAAGACUGACU	146	2633	AGUCAGUCUUUUAUUAUCAGA	573
2629	UACCUAUAUAAUUAUUGG	147	2629	UACCUAUAUAAUUAUUGG	147	2651	CCAUUAUAAUUGAUAGGUA	574
2647	GACCCAGAUAAGUUCUUU	148	2647	GACCCAGAUAAGUUCUUU	148	2669	AAGGAACUUAUCUGGGUC	575
2665	UUGGAUGAGCAGUGAGC	149	2665	UUGGAUGAGCAGUGAGC	149	2687	GCUCACACUGCUCAUCCAA	576
2683	CGGCUCCUUAUGGCCA	150	2683	CGGCUCCUUAUGGCCA	150	2705	UGGCAUCAUAAAGGAGCGG	577
2701	AGCAUGGGAGUUUGCCC	151	2701	AGCAUGGGAGUUUGCCC	151	2723	GGGCAACUCCACUUGCU	578
2719	CGGGAGAGACUUAACUGG	152	2719	CGGGAGAGACUUAACUGG	152	2741	CCAGUUUAAUGUCUCUCCCG	579
2737	GGCAAAACACUUGGAAGAG	153	2737	GGCAAAACACUUGGAAGAG	153	2759	CUCUCCAAAGUGAUUUGCC	580
2755	GGGGCUUUUGGAAAAGUGG	154	2755	GGGGCUUUUGGAAAAGUGG	154	2777	CCACUUUCCAAAAGCCCC	581
2773	GUUCAAGCAUCAGCAUUUG	155	2773	GUUCAAGCAUCAGCAUUUG	155	2795	CAAAUGCUGAUGCUUGAAC	582
2791	GGCAUUAAGAAUACCCUA	156	2791	GGCAUUAAGAAUACCCUA	156	2813	UAGGUGAUUUCUUAUUGCC	583
2809	ACGUGCCGACUUGGCGUG	157	2809	ACGUGCCGACUUGGCGUG	157	2831	CAGCCACAGUCCGGCACGU	584
2827	GUGAAAUGCUGAAAGAGG	158	2827	GUGAAAUGCUGAAAGAGG	158	2849	CCUCUUUCAGCAUUUUCAC	585
2845	GGGGCCACGGCCAGCGAGU	159	2845	GGGGCCACGGCCAGCGAGU	159	2867	ACUCGUGGCCGUGGGCCCC	586
2863	UACAAAGCUCUGAUGACUG	160	2863	UACAAAGCUCUGAUGACUG	160	2885	CAGUCAUCAGAGCUUUGUA	587
2881	GAGCUAAAAUUCUUGACCC	161	2881	GAGCUAAAAUUCUUGACCC	161	2903	GGGUCAGAUAUUUUAAGCUC	588
2899	CACAUUGGCCACCAUCUGA	162	2899	CACAUUGGCCACCAUCUGA	162	2921	UCAGAUUGGUGGCCAAUGUG	589
2917	AACGUGGUUAACCUUGCUGG	163	2917	AACGUGGUUAACCUUGCUGG	163	2939	CCAGCAGGUUAACCAACGUU	590
2935	GGAGCCUGCACCAAGCAAG	164	2935	GGAGCCUGCACCAAGCAAG	164	2957	CUUGCUUUGGUGCAGGCUCUC	591
2953	GGAGGGCCUCUGAUGGUGA	165	2953	GGAGGGCCUCUGAUGGUGA	165	2975	UCACCAUCAGAGGCCCUCC	592
2971	AUUGUUGAAUACUGCAAAU	166	2971	AUUGUUGAAUACUGCAAAU	166	2993	AUUUGCAGUAUUAACAUAU	593
2989	UAUGGAAUUCUCUCCAAU	167	2989	UAUGGAAUUCUCUCCAAU	167	3011	AGUUGGAGAGAUUUAUUAU	594
3007	UACCUCAAGAGCAAAACGUG	168	3007	UACCUCAAGAGCAAAACGUG	168	3029	CACGUUUGCUCUUGAGGUA	595
3025	GACUUAUUUUUUCUCAACA	169	3025	GACUUAUUUUUUCUCAACA	169	3047	UGUUGAGAAAAAAUAAGUC	596
3043	AAGGAUGCAGCACUACACA	170	3043	AAGGAUGCAGCACUACACA	170	3065	UGUGUAGUGCUGCAUCCUU	597
3061	AUGGAGCCUAGAAAGAAA	171	3061	AUGGAGCCUAGAAAGAAA	171	3083	UUUCUUUCUUAAGGCUCCAU	598
3079	AAAUGGAGCCAGGCCUGG	172	3079	AAAUGGAGCCAGGCCUGG	172	3101	CCAGGCCUGGCCUCCAUUUU	599
3097	GAACAAGGCAAGAAACCAA	173	3097	GAACAAGGCAAGAAACCAA	173	3119	UUGGUUUCUUGCCUUGUUC	600
3115	AGACUAGAUAGCGUACCCA	174	3115	AGACUAGAUAGCGUACCCA	174	3137	UGGUGACGCUAUCUAGUCU	601

3133	AGCAGCGAAAGCUUUGCGA	175	3133	AGCAGCGAAAGCUUUGCGA	175	3155	UCGCAAAAGCUUUGCGUCU	602
3151	AGCUCGGCUUUCAGGAAG	176	3151	AGCUCGGCUUUCAGGAAG	176	3173	CUUCCUGAAAGCCGGAGCU	603
3169	GAUAAAAGUCUGAGUGAUG	177	3169	GAUAAAAGUCUGAGUGAUG	177	3191	CAUCACUCAGACUUUUAUC	604
3187	GUUGAGGAAGAGGAGGAUU	178	3187	GUUGAGGAAGAGGAGGAUU	178	3209	AAUCCUCCUCUCCUCAAC	605
3205	UCUGACGGUUUCUACAAGG	179	3205	UCUGACGGUUUCUACAAGG	179	3227	CCUUGUAGAAACCGUCAGA	606
3223	GAGCCCAUCACUAUGGAAG	180	3223	GAGCCCAUCACUAUGGAAG	180	3245	CUUCCAUAGUGAUGGGCUC	607
3241	GAUCUGAUUUUCUACAGUU	181	3241	GAUCUGAUUUUCUACAGUU	181	3263	AACUGUAGAAAUACAGAU	608
3259	UUUCAAUGGGCCAGAGGCA	182	3259	UUUCAAUGGGCCAGAGGCA	182	3281	UGCCUCUGGCCACUUGAAA	609
3277	AUGGAGUCCUGUCUCCA	183	3277	AUGGAGUCCUGUCUCCA	183	3299	UGGAAGACAGGAACUCCA	610
3295	AGAAUGGCAUUAUCGGG	184	3295	AGAAUGGCAUUAUCGGG	184	3317	CCCGAUGAAUGCACUUCU	611
3313	GACCUGGACGAGAAACA	185	3313	GACCUGGACGAGAAACA	185	3335	UGUUUCUCGCGGCCAGGUC	612
3331	AUUCUUUAUCUGAGAACA	186	3331	AUUCUUUAUCUGAGAACA	186	3353	UGUUCUCAGAUAAAAGAU	613
3349	AACGUGGUGAAGAUUUGUG	187	3349	AACGUGGUGAAGAUUUGUG	187	3371	CACAAACUUCACCCACGU	614
3367	GAUUUGGCCUUGCCCGGG	188	3367	GAUUUGGCCUUGCCCGGG	188	3389	CCCGGGCAAGGCCAAAUUC	615
3385	GAUUAUUAAGAACCCCGG	189	3385	GAUUAUUAAGAACCCCGG	189	3407	CGGGGUUCUUAUAAAUAUC	616
3403	GAUAUGUGAGAAAAGGAG	190	3403	GAUAUGUGAGAAAAGGAG	190	3425	CUCUUUUUCUCACAUAAUC	617
3421	GAUACUCGACUCCUCUGA	191	3421	GAUACUCGACUCCUCUGA	191	3443	UCAGGGAAAGUCGAGUAUC	618
3439	AAUUGGAUGGCCUCCCGAAU	192	3439	AAUUGGAUGGCCUCCCGAAU	192	3461	AUUCGGGAGCCAUCCAUUU	619
3457	UCUAUCUUIUGACAAAUCU	193	3457	UCUAUCUUIUGACAAAUCU	193	3479	AGAUUUUGUCAAAGAUAGA	620
3475	UACAGCACCAAGAGCGACG	194	3475	UACAGCACCAAGAGCGACG	194	3497	CGUCGCUUUGGUGGUGUA	621
3493	GUGUGGUCUUAACGGAGUAU	195	3493	GUGUGGUCUUAACGGAGUAU	195	3515	AUACUCCGUAAAGACCACAC	622
3511	UUGCUGUGGGAAUUCUUCU	196	3511	UUGCUGUGGGAAUUCUUCU	196	3533	AGAAGAUUUCGCCACAGCAA	623
3529	UCCUAGGUGGGUCUCUCCAU	197	3529	UCCUAGGUGGGUCUCUCCAU	197	3551	AUGGAGACCCACCUCUAGGA	624
3547	UACCCAGGAGUACAAAUGG	198	3547	UACCCAGGAGUACAAAUGG	198	3569	CCAUUUGUACUCCUGGGUA	625
3565	GAUGAGGACUUAUUGCAGUC	199	3565	GAUGAGGACUUAUUGCAGUC	199	3587	GACUGCAAAAGUCCUCAUC	626
3583	CGCCUGAGGGAAGGCAUGA	200	3583	CGCCUGAGGGAAGGCAUGA	200	3605	UCAUGCCUCCUCCAGGGCG	627
3601	AGGAUGAGAGCUCUUGAGU	201	3601	AGGAUGAGAGCUCUUGAGU	201	3623	ACUCAGGAGCUCUCAUCCU	628
3619	UACUCUACUCCUGAAAUCU	202	3619	UACUCUACUCCUGAAAUCU	202	3641	AGAUUUCAGGAGUAGAGUA	629
3637	UAUCAGAUCAUGCUGGACU	203	3637	UAUCAGAUCAUGCUGGACU	203	3659	AGUCCAGCAUGAUCUGAUA	630
3655	UGCUGGCACAGAGACCCAA	204	3655	UGCUGGCACAGAGACCCAA	204	3677	UUGGGUCUCUGUGGCCAGCA	631
3673	AAAGAAAGCCAAAGAUUUG	205	3673	AAAGAAAGCCAAAGAUUUG	205	3695	CAAAUCUUGGCCUUCUUCU	632
3691	GCAGAAUUGUGGAAAAAC	206	3691	GCAGAAUUGUGGAAAAAC	206	3713	GUUUUCCACAAAGUUCUGC	633
3709	CUAGGUGAUUUGCUUCAAG	207	3709	CUAGGUGAUUUGCUUCAAG	207	3731	CUUGAAGCAAAUACCUAG	634
3727	GCAAAUGUACAACAGGAUG	208	3727	GCAAAUGUACAACAGGAUG	208	3749	CAUCCUGUUGUACAUIUUGC	635
3745	GGUAAAAGACUACAUCCCAA	209	3745	GGUAAAAGACUACAUCCCAA	209	3767	UUGGGAUGUAGUCUUAUACC	636
3763	AUCAAUGCCAUACUGACAG	210	3763	AUCAAUGCCAUACUGACAG	210	3785	CUGUCAGUAUGGCAUUGAU	637

3781	GGAAUAGUGGGUUUACAU	211	3781	GGAAUAGUGGGUUUACAU	211	3803	AUGUAAACCCACUAAUUC	638
3799	UACUCAACUCCUGCCUUCU	212	3799	UACUCAACUCCUGCCUUCU	212	3821	AGAAGGCAGGAGUUAGUA	639
3817	UCUGAGGACUUCUUAAGG	213	3817	UCUGAGGACUUCUUAAGG	213	3839	CCUUGAAGAAAGUCCUCAGA	640
3835	GAAAGUAAUUCAGCUCCGA	214	3835	GAAAGUAAUUCAGCUCCGA	214	3857	UCGGAGCUGAAAUACUUUC	641
3853	AAGUUAAUUCAGGAAGCU	215	3853	AAGUUAAUUCAGGAAGCU	215	3875	AGCUUCCUGAAUUAAACUU	642
3871	UCUGAUGAUCAGAUUAG	216	3871	UCUGAUGAUCAGAUUAG	216	3893	CAUAUCUGACAUCAUCAGA	643
3889	GUAAUGCUUUAAGUUCA	217	3889	GUAAUGCUUUAAGUUCA	217	3911	UGAACUUUGAAAGCAUUUAC	644
3907	AUGAGCCUGGAAAGAAUCA	218	3907	AUGAGCCUGGAAAGAAUCA	218	3929	UGAUUUCUUUCCAGGCUCAU	645
3925	AAAACCUUUGAAGAACUUU	219	3925	AAAACCUUUGAAGAACUUU	219	3947	AAAGUUUCUUCAAAAGGUUUU	646
3943	UUACCGAAUCCACCUCCA	220	3943	UUACCGAAUCCACCUCCA	220	3965	UGGAGGUGGCAUUUCGGUAA	647
3961	AUGUUUGAUCUACCCAGG	221	3961	AUGUUUGAUCUACCCAGG	221	3983	CCUGGUAUCUCAAACAU	648
3979	GGGACAGCAGCACUCUCUG	222	3979	GGGACAGCAGCACUCUCUG	222	4001	ACAGAGUCGUCGUGUCGCC	649
3997	UUGGCCUCUCCCAUGCUGA	223	3997	UUGGCCUCUCCCAUGCUGA	223	4019	UCAGCAUGGGAGAGGCCAA	650
4015	AAGCGCUACCCUGGACUG	224	4015	AAGCGCUACCCUGGACUG	224	4037	CAGUCCAGGUGAAGCGCUU	651
4033	GACAGCAAAACCCAAAGCCU	225	4033	GACAGCAAAACCCAAAGCCU	225	4055	AGCCUUUGGGUUUUGCUGUC	652
4051	UCGCUCAAGAUUGACUUGA	226	4051	UCGCUCAAGAUUGACUUGA	226	4073	UCAAGUCAUUCUUGAGCGA	653
4069	AGAGUAACCCAGUAAAAGUA	227	4069	AGAGUAACCCAGUAAAAGUA	227	4091	UACUUUACUGGUUACUCU	654
4087	AAGGAGUCGGGCGUGUCUG	228	4087	AAGGAGUCGGGCGUGUCUG	228	4109	CAGACAGCCCCGACUCCUU	655
4105	GAUGUCAGCAGGCCCCAGUU	229	4105	GAUGUCAGCAGGCCCCAGUU	229	4127	AACUGGGCGUCGUCACAU	656
4123	UUCUGCCAUUCCAGCUGUG	230	4123	UUCUGCCAUUCCAGCUGUG	230	4145	CACAGCUGGAUUGGCAGAA	657
4141	GGGCACGUCAGCGAAGGCA	231	4141	GGGCACGUCAGCGAAGGCA	231	4163	UGCCUUCGUCGACGUGCCC	658
4159	AAGCGCAGGUUACCCUACG	232	4159	AAGCGCAGGUUACCCUACG	232	4181	CGUAGGUGAACCCUGCGCUU	659
4177	GACCACGUCAGCUGGAAA	233	4177	GACCACGUCAGCUGGAAA	233	4199	UUUCCAGCUCAGCGUGGUC	660
4195	AGGAAAUUCGCGUGCUGCU	234	4195	AGGAAAUUCGCGUGCUGCU	234	4217	AGCAGCACGCGAUUUUCCU	661
4213	UCCCGCCCCCAGACUACA	235	4213	UCCCGCCCCCAGACUACA	235	4235	UGUAGUCUGGGGGCGGGGA	662
4231	AACUGGUGGUCCUGUACU	236	4231	AACUGGUGGUCCUGUACU	236	4253	AGUACAGGACCACCGAGUU	663
4249	UCCACCCACCCAUUCUAGA	237	4249	UCCACCCACCCAUUCUAGA	237	4271	UCUAGAUUGGGUGGGGUGGA	664
4267	AGUUUGACACGAAGCCUUA	238	4267	AGUUUGACACGAAGCCUUA	238	4289	UAAGGCUUCGUGUCAAAACU	665
4285	AUUUCUAGAAACACAUUG	239	4285	AUUUCUAGAAACACAUUG	239	4307	CACAUUGUCUUCUAGAAAU	666
4303	GUUUUUAUACCCCCAGGAA	240	4303	GUUUUUAUACCCCCAGGAA	240	4325	UUCUUGGGGUAUAAAUAC	667
4321	AACUAGCUUUUGCCAGUUA	241	4321	AACUAGCUUUUGCCAGUUA	241	4343	AUACUGGCAAAAGCUAGUU	668
4339	UUUUGCAUUAUUAAGUUUA	242	4339	UUUUGCAUUAUUAAGUUUA	242	4361	UAAACUUUAUUAUUGCAUAA	669
4357	ACACCUUUAUCUUUCCAU	243	4357	ACACCUUUAUCUUUCCAU	243	4379	CAUGGAAAGAUAAAAGUGU	670
4375	GGGAGCCAGCUGCUUUUUG	244	4375	GGGAGCCAGCUGCUUUUUG	244	4397	CAAAAAGCAGCUGGCUCCC	671
4393	GUGAUUUUUUUUAUAGUGC	245	4393	GUGAUUUUUUUUAUAGUGC	245	4415	GCACUUAUAAAAAUACAC	672
4411	CUUUUUUUUUUUUGACUAC	246	4411	CUUUUUUUUUUUUGACUAC	246	4433	GUUAGUCAAAAAAAAAG	673

4429	CAAGAAUGUAACUCCAGAU	247	4429	CAAGAAUGUAACUCCAGAU	247	4451	AUCUGGAGUUAUUAUUCUUG	674
4447	UAGAGAAAUAGUGACAAGU	248	4447	UAGAGAAAUAGUGACAAGU	248	4469	ACUUGUCACUUAUUCUCUA	675
4465	UGAAGAACACUACUGCUAA	249	4465	UGAAGAACACUACUGCUAA	249	4487	UUAGCAGUAGUUGUUCUUA	676
4483	AAUCCUCAUGUUAUCUCAGU	250	4483	AAUCCUCAUGUUAUCUCAGU	250	4505	ACUGAGUAAACUAGAGGAUU	677
4501	UGUUAGAGAAAUCCUUCU	251	4501	UGUUAGAGAAAUCCUUCU	251	4523	AGGAAGGUAUUCUCUAACA	678
4519	UAAACCCAAUGACUUCUCCU	252	4519	UAAACCCAAUGACUUCUCCU	252	4541	AGGGAAGUCUUAUGGGUUA	679
4537	UGCUCCAAACCCCGCCACC	253	4537	UGCUCCAAACCCCGCCACC	253	4559	GGUGGCGGGGUUGGAGCA	680
4555	CUCAGGACACGACGACCA	254	4555	CUCAGGACACGACGACCA	254	4577	UGGUCCUGCGUGGCCUGAG	681
4573	AGUUUGAUUGAGGAGCUGC	255	4573	AGUUUGAUUGAGGAGCUGC	255	4595	GCAGCUCCUCAUAUCAAACU	682
4591	CACUGAUCACCCAAUGCAU	256	4591	CACUGAUCACCCAAUGCAU	256	4613	AUGCAUUGGGGUGAUCAGUG	683
4609	UCACGUACCCACUGGGCC	257	4609	UCACGUACCCACUGGGCC	257	4631	GGCCAGUGGGGUACGUGA	684
4627	CAGCCUGCAGCCCAAAAC	258	4627	CAGCCUGCAGCCCAAAAC	258	4649	GUUUUGGGCUGCAGGGCUG	685
4645	CCAGGGCAACAAGCCCGU	259	4645	CCAGGGCAACAAGCCCGU	259	4667	ACGGGCUUGUUGCCCGGG	686
4663	UUAAGCCCAAGGGGAUCACU	260	4663	UUAAGCCCAAGGGGAUCACU	260	4685	AGUGAUCCCUUGGGGCUAA	687
4681	UGGUGGGCUGAGCAACAU	261	4681	UGGUGGGCUGAGCAACAU	261	4703	AUGUUGCUCAGGCCAGCCA	688
4699	UCUGGGGAGUCCUCUAGCA	262	4699	UCUGGGGAGUCCUCUAGCA	262	4721	UGCUAGAGACUCCCGGAGA	689
4717	AGGCCUAGACAUUGUGAGG	263	4717	AGGCCUAGACAUUGUGAGG	263	4739	CCUCAGAGUCUUAAGCCU	690
4735	GAGGAAAAGGAAAAAAGC	264	4735	GAGGAAAAGGAAAAAAGC	264	4757	GCUUUUUUCCUUUUUCCUC	691
4753	CAAAAAGCAAGGGAGAAAA	265	4753	CAAAAAGCAAGGGAGAAAA	265	4775	UUUUCUCCCUUGGCUUUUUG	692
4771	AGAGAAACCGGAGAAAGC	266	4771	AGAGAAACCGGAGAAAGC	266	4793	GCUUUCUCCCGGUUUUCUCU	693
4789	CAUGAGAAAGAAUUUGAGA	267	4789	CAUGAGAAAGAAUUUGAGA	267	4811	UCUCAAUUUCUUUCUUG	694
4807	ACGCACCAUGUGGGCACGG	268	4807	ACGCACCAUGUGGGCACGG	268	4829	CCGUCCCAUUGGUGGCGU	695
4825	GAGGGGACGGGGCUCAGC	269	4825	GAGGGGACGGGGCUCAGC	269	4847	GCUGAGCCCGUCCCGCCUC	696
4843	CAAUGCCAUUUCAGUGGCU	270	4843	CAAUGCCAUUUCAGUGGCU	270	4865	AGCCACUGAAAUGGCAUUG	697
4861	UUCCAGCUCUGACCCUUC	271	4861	UUCCAGCUCUGACCCUUC	271	4883	GAAAGGUCAGAGCGUGGAA	698
4879	CUACAUUUGAGGGCCACG	272	4879	CUACAUUUGAGGGCCACG	272	4901	GCUGGGCCCUCAAUUGUAG	699
4897	CCAGGAGCAGAUUGGACAGC	273	4897	CCAGGAGCAGAUUGGACAGC	273	4919	GCUGUCCAUUGCUCCUGG	700
4915	CGAUGAGGGGACAUUUUCU	274	4915	CGAUGAGGGGACAUUUUCU	274	4937	AGAAAAUGUCCCGCUAUCG	701
4933	UGGAUUCUGGGAGGCAAGA	275	4933	UGGAUUCUGGGAGGCAAGA	275	4955	UCUUGCCUCCCGAGAAUCCA	702
4951	AAAAGGACAAAUAUCUUUU	276	4951	AAAAGGACAAAUAUCUUUU	276	4973	AAAAGAUUUUGUCCUUUU	703
4969	UUUGGAACUAAAGCAAAUU	277	4969	UUUGGAACUAAAGCAAAUU	277	4991	AAUUUGCUUUAUUGUCCAAA	704
4987	UUUAGACCUUUUACCUAUGG	278	4987	UUUAGACCUUUUACCUAUGG	278	5009	CCAUAGGUAAAAGGUCUAAA	705
5005	GAAUGGUUUCUAUGUCCAU	279	5005	GAAUGGUUUCUAUGUCCAU	279	5027	AUGGACAUAGAACACACUUC	706
5023	UUCUCAUUCGUGGCAUGUU	280	5023	UUCUCAUUCGUGGCAUGUU	280	5045	AACAUGGCCACGAAUGAGAA	707
5041	UUUGAUUUUGUAGCACUGAG	281	5041	UUUGAUUUUGUAGCACUGAG	281	5063	CUCAGUGCUACAAAUCAAAA	708
5059	GGGUGGCACUCAACUCUGA	282	5059	GGGUGGCACUCAACUCUGA	282	5081	UCAGAGUUUGAGUGCCACCC	709

5077	AGCCCAUACUUUUGGCUC	283	5077	AGCCCAUACUUUUGGCUC	283	5099	GGAGCCAAAAGUAUUGGCU	710
5095	CUCUAGUAAGACACUGA	284	5095	CUCUAGUAAGACACUGA	284	5117	UCAGUGCAUCUUAACUAG	711
5113	AAAACUUAGCCAGAGUAG	285	5113	AAAACUUAGCCAGAGUAG	285	5135	CUAACUCUGGCUAAGUUU	712
5131	GGUUGUCUCCAGGCCAUGA	286	5131	GGUUGUCUCCAGGCCAUGA	286	5153	UCAUGGCCUGGAGACAACC	713
5149	AUGGCCUUACACUGAAAAU	287	5149	AUGGCCUUACACUGAAAAU	287	5171	AUUUCAGUGUAAGGCCAU	714
5167	UGUCACAUUCUUAUUUGG	288	5167	UGUCACAUUCUUAUUUGG	288	5189	CCCAAAUAGAAUGUGACA	715
5185	GUUUUAUUAUAGUCCAG	289	5185	GUUUUAUUAUAGUCCAG	289	5207	CUGGACUAUAUUAUUAAC	716
5203	GACACUUAACUAAUUUCU	290	5203	GACACUUAACUAAUUUCU	290	5225	AGAAUUUGAGUUAAGUGUC	717
5221	UUGGUUAUUUCUGUUUUG	291	5221	UUGGUUAUUUCUGUUUUG	291	5243	CAAAACAGAAUAAUACCAA	718
5239	GCACAGUUAUUGUGAAAG	292	5239	GCACAGUUAUUGUGAAAG	292	5261	CUUUCACAACUAAACUGUGC	719
5257	GAAUGCAGUAGAGGAGAA	293	5257	GAAUGCAGUAGAGGAGAA	293	5279	UUCAUUCUUCACAGCUUUC	720
5275	AAUUGCAGUAGAGGAGAA	294	5275	AAUUGCAGUAGAGGAGAA	294	5297	UCUCCUCAGGACUGCAUUU	721
5293	AGUUUCUCCAUUAUAAAA	295	5293	AGUUUCUCCAUUAUAAAA	295	5315	UUUUGAUUGGAGAAAACU	722
5311	ACGAGGCCUGAUGGAGAA	296	5311	ACGAGGCCUGAUGGAGAA	296	5333	UUCUCCCAUCAGCCUCUGU	723
5329	AAAAGGUCAUAAGGUCAA	297	5329	AAAAGGUCAUAAGGUCAA	297	5351	UUGACCUUAUUGACCUUUU	724
5347	AGGGAAGACCCCGUCUCUA	298	5347	AGGGAAGACCCCGUCUCUA	298	5369	UAGAGACGGGUCUUCUCCU	725
5365	AUACCAACCAAAACCAUUC	299	5365	AUACCAACCAAAACCAUUC	299	5387	GAAUUGUUUGGUUGGUUAU	726
5383	CACCAACACAGUUGGGACC	300	5383	CACCAACACAGUUGGGACC	300	5405	GGUCCCAACUGUUUGGUG	727
5401	CCAAAACACAGGAAGUCAG	301	5401	CCAAAACACAGGAAGUCAG	301	5423	CUGACUUCUGUGUUUUGG	728
5419	GUCACGUUCCUUUUCAUU	302	5419	GUCACGUUCCUUUUCAUU	302	5441	AUAGAAAAGAAACGUGAC	729
5437	UUAAUGGGGAUCCACUUA	303	5437	UUAAUGGGGAUCCACUUA	303	5459	AUAGUGGAUACCCCAUUA	730
5455	UCUCACACUAAUCUGAAAG	304	5455	UCUCACACUAAUCUGAAAG	304	5477	CUUUCAGAUUAGUGUGAGA	731
5473	GGAUGUGGAAGAGCAUUA	305	5473	GGAUGUGGAAGAGCAUUA	305	5495	CUAAUGCUCUCCACAUCC	732
5491	GCUGGCGCAUUAUUAAGCAC	306	5491	GCUGGCGCAUUAUUAAGCAC	306	5513	GUGCUUAAUUAUGCGCCAGC	733
5509	CUUUAAGCUCUUGAGUAA	307	5509	CUUUAAGCUCUUGAGUAA	307	5531	UUACUCAAAGGAGCUIAAAG	734
5527	AAAAGGUGGUUUAUUAUUU	308	5527	AAAAGGUGGUUUAUUAUUU	308	5549	AAAUUACAUACCAUUAUU	735
5545	UAUGCAAGGUUUAUUCUCCA	309	5545	UAUGCAAGGUUUAUUCUCCA	309	5567	UGGAGAAAUACCUUGCAUA	736
5563	AGUUGGGACUCAGGAUUAU	310	5563	AGUUGGGACUCAGGAUUAU	310	5585	AAUAUCCUGAGUCCCAACU	737
5581	UAGUUAAUAGAGCCAUACU	311	5581	UAGUUAAUAGAGCCAUACU	311	5603	AGUGAUGGCUCAUUAACUA	738
5599	UAGAAAGAAAGCCCAUUUU	312	5599	UAGAAAGAAAGCCCAUUUU	312	5621	AAAAUGGGCUUUUUCUUA	739
5617	UACACUGCUUUGAAACUUG	313	5617	UACACUGCUUUGAAACUUG	313	5639	CAAGUUUCAAAGAGUUGA	740
5635	GCCUGGGGUCUGAGCAUGA	314	5635	GCCUGGGGUCUGAGCAUGA	314	5657	UCAUGCUCAGACCCAGGC	741
5653	AUGGAAUAGGGAGACAGG	315	5653	AUGGAAUAGGGAGACAGG	315	5675	CCUGUCUCCCUUUCUCCAU	742
5671	GGUAGGAAAGGGCGCCUAC	316	5671	GGUAGGAAAGGGCGCCUAC	316	5693	GUAGGCGCCCUUUCUACC	743
5689	CUCUUCAGGGUUAUUAAGAU	317	5689	CUCUUCAGGGUUAUUAAGAU	317	5711	AUCUUUAGACCCUGAAGAG	744
5707	UCAAGUGGGCCUUGGAUCG	318	5707	UCAAGUGGGCCUUGGAUCG	318	5729	CGAUCCAAAGGCCACUUGA	745

5725	GCUAAGCUGGCUCUGUUUG	319	5725	GCUAAGCUGGCUCUGUUUG	319	5747	CAACAGAGCCAGCUUAGC	746
5743	GAUGCUAUUUAUGCAAGUU	320	5743	GAUGCUAUUUAUGCAAGUU	320	5765	AACUUGCAUAAUAGCAUC	747
5761	UAGGGUCUAUGUAUUUAGG	321	5761	UAGGGUCUAUGUAUUUAGG	321	5783	CCUAAUUAUAGACCCUA	748
5779	GAUGGCCUACUCUUCAGG	322	5779	GAUGGCCUACUCUUCAGG	322	5801	CCUGAAGAGUAGGCGCAUC	749
5797	GGUCUAAAGAUCAAGUGGG	323	5797	GGUCUAAAGAUCAAGUGGG	323	5819	CCCACUUGAUUUUAGACC	750
5815	GCCUUGGUAUCUAAGCUG	324	5815	GCCUUGGUAUCUAAGCUG	324	5837	CAGCUUAGCGAUCCAAGGC	751
5833	GGCUCUGUUUGAUGCUAUU	325	5833	GGCUCUGUUUGAUGCUAUU	325	5855	AAUAGCAUCAAACAGAGCC	752
5851	UUAUGCAAGUUAAGGUCUA	326	5851	UUAUGCAAGUUAAGGUCUA	326	5873	UAGACCCUAAACUUGCAUA	753
5869	AUGUAUUUAGGAUGUCUG	327	5869	AUGUAUUUAGGAUGUCUG	327	5891	GCAGACAUCUAAAUACA	754
5887	CACCUUCUGAGCCAGUCA	328	5887	CACCUUCUGAGCCAGUCA	328	5909	UGACUGGCUGCAGAAAGGUG	755
5905	AGAAGCUGGAGAGGCAACA	329	5905	AGAAGCUGGAGAGGCAACA	329	5927	UGUUGCCUCUCCAGCUUCU	756
5923	AGUGGAUUGCUCUUCUUG	330	5923	AGUGGAUUGCUCUUCUUG	330	5945	CAAGAAGCAGCAAUCCACU	757
5941	GGGGAGAGAGUAUCUUC	331	5941	GGGGAGAGAGUAUCUUC	331	5963	GAAGCAUACUCUUCUCCCC	758
5959	CCUUUUUUAUCCAUUAUUU	332	5959	CCUUUUUUAUCCAUUAUUU	332	5981	AAAUACAUGGAUAAAGG	759
5977	UAACUGUAGAACCUGAGCU	333	5977	UAACUGUAGAACCUGAGCU	333	5999	AGCUCAGGUUCUACAGUUA	760
5995	UCUAAGUAACCGAAGAAUG	334	5995	UCUAAGUAACCGAAGAAUG	334	6017	CAUUCUUGGUUAUCUUA	761
6013	GUAGCCUCUGUUCUUAUG	335	6013	GUAGCCUCUGUUCUUAUG	335	6035	CAUAAACAGAGGCAUAC	762
6031	GUGCCACAUCUUGUUUAA	336	6031	GUGCCACAUCUUGUUUAA	336	6053	UUAAACAAGGAUGUGGCAC	763
6049	AAGGCUCUCUGUAUGAAGA	337	6049	AAGGCUCUCUGUAUGAAGA	337	6071	UCUUCAUACAGAGAGCCUU	764
6067	AGAUGGACCGUCAUCAGC	338	6067	AGAUGGACCGUCAUCAGC	338	6089	GCUGAUGACGGUCCCAUCU	765
6085	CACAUUCCUAGUGAGCCU	339	6085	CACAUUCCUAGUGAGCCU	339	6107	AGGCUCACUAGGGAAUGUG	766
6103	UACUGGCUCUUGGCAGCGG	340	6103	UACUGGCUCUUGGCAGCGG	340	6125	CCGCUGCCAGGAGCCAGUA	767
6121	GCUUUUGUGGAAGACUCAC	341	6121	GCUUUUGUGGAAGACUCAC	341	6143	GUGAGUCUUCACAAAGC	768
6139	CUAGCCAGAGAGAGGAGU	342	6139	CUAGCCAGAGAGAGGAGU	342	6161	ACUCCUCUCUUGGCUAG	769
6157	UGGGACAGUCCUCCACC	343	6157	UGGGACAGUCCUCCACC	343	6179	GGUGGAGAGGACUGUCCCA	770
6175	CAAGAUCAAUCCAAACA	344	6175	CAAGAUCAAUCCAAACA	344	6197	UGUUUGGAUUUAGAUCUUG	771
6193	AAAGCAGGCUAGAGCCAG	345	6193	AAAGCAGGCUAGAGCCAG	345	6215	CUGGCUCUAGCCUGCUUUU	772
6211	GAAGAGAGGACAAUUCUUU	346	6211	GAAGAGAGGACAAUUCUUU	346	6233	AAAGAUUUGUCCUCUCUUC	773
6229	UGUUUUCUUCUUCUUUAC	347	6229	UGUUUUCUUCUUCUUUAC	347	6251	GUAAAGAAGAGGAACAACA	774
6247	CACAUACGAAACACCUG	348	6247	CACAUACGAAACACCUG	348	6269	CAGGUGGUUUGCGUAUGUG	775
6265	GUGACAGCUGGCAUUUUUA	349	6265	GUGACAGCUGGCAUUUUUA	349	6287	UAAAAUUGCCAGCUGUCAC	776
6283	AUAAUACAGGUACUGGAA	350	6283	AUAAUACAGGUACUGGAA	350	6305	UCCAGUUUACCUGAUUUU	777
6301	AGGAGGUUAAACUCAGAAA	351	6301	AGGAGGUUAAACUCAGAAA	351	6323	UUUCUGAGUUUAAACCUCCU	778
6319	AAAAGAAACCUACAGUCAA	352	6319	AAAAGAAACCUACAGUCAA	352	6341	UUACUGAGGUCUUCUUUUU	779
6337	AUUCUCUACUUUUUUUUUU	353	6337	AUUCUCUACUUUUUUUUUU	353	6359	AAAAAAAAGUAGAGAAU	780
6355	UUUUUUUCCAAUACAGAU	354	6355	UUUUUUUCCAAUACAGAU	354	6377	UAUCUGAUUUUGGAAAAAA	781

6373	AAUAGCCCAGCAAAUAGUG	355	6373	AAUAGCCCAGCAAAUAGUG	355	6395	CACUAAUUGCUGGGCUAUU	782
6391	GAUAAACAAUAAACCCUUA	356	6391	GAUAAACAAUAAACCCUUA	356	6413	UAAGGUUUUAUUUGUUAUC	783
6409	AGCUGUUCAGUCUUGAUU	357	6409	AGCUGUUCAGUCUUGAUU	357	6431	AAUCAAGACAUGAACAGCU	784
6427	UUCAAUAAUAAUUCUUA	358	6427	UUCAAUAAUAAUUCUUA	358	6449	UUAAGAAUUAUUUAUGAA	785
6445	AUCAUUAAGAGACCAUAAU	359	6445	AUCAUUAAGAGACCAUAAU	359	6467	AUUAUGGUCUCUUAUUGAU	786
6463	UAAUACUCCUUUUAAGA	360	6463	UAAUACUCCUUUUAAGA	360	6485	UCUUGAAAAGGAGUAUUUA	787
6481	AGAAAAGCAAAACCAUUA	361	6481	AGAAAAGCAAAACCAUUA	361	6503	CUAAGGUUUUGCUUUUCU	788
6499	GAUUGUUACUCAGCUCCU	362	6499	GAUUGUUACUCAGCUCCU	362	6521	AGGAGCUGAGUAACAAUUC	789
6517	UUCAAACUCAGGUUUGUAG	363	6517	UUCAAACUCAGGUUUGUAG	363	6539	CUACAAACCCUGAGUUUGAA	790
6535	GCAUACAUGAGUCCAUC	364	6535	GCAUACAUGAGUCCAUC	364	6557	UGGAUGGACUCUUAUGC	791
6553	AUCAGUCAAGAAUGGUUC	365	6553	AUCAGUCAAGAAUGGUUC	365	6575	GAACCAUUCUUUGACUGAU	792
6571	CCAUCUGGAGUCUUUAUGU	366	6571	CCAUCUGGAGUCUUUAUGU	366	6593	ACAUUAAGACUCCAGAUUG	793
6589	UAGAAAGAAAUGGAGAC	367	6589	UAGAAAGAAAUGGAGAC	367	6611	GUCUCCAUUUUUCUUUCUA	794
6607	CUUGUAUUAUGAGCUAGU	368	6607	CUUGUAUUAUGAGCUAGU	368	6629	ACUAGCUCAUUAUUACAAG	795
6625	UUACAAAGUGCUUUGUUAU	369	6625	UUACAAAGUGCUUUGUUAU	369	6647	AUGAACAAAGCACUUUUGUA	796
6643	UUAAAAUAGCUCUGAAAAU	370	6643	UUAAAAUAGCUCUGAAAAU	370	6665	AUUUACAGUCUUAUUUUA	797
6661	UUGAAACAUGAAUUAACUG	371	6661	UUGAAACAUGAAUUAACUG	371	6683	CAGUAAUUCUUAUUUCAA	798
6679	GAUAAUUAUCCAUUAUUU	372	6679	GAUAAUUAUCCAUUAUUU	372	6701	AAUUGUUGGAUUAUUUAUC	799
6697	UGCCAUUUUAUACAAAAU	373	6697	UGCCAUUUUAUACAAAAU	373	6719	UUUUUGUCAUAAUUGGCA	800
6715	UGGUUGGCACUACAAAGA	374	6715	UGGUUGGCACUACAAAGA	374	6737	UUUUUGUUAUGUCCCAACCA	801
6733	AACGAGCACUCCUUCAG	375	6733	AACGAGCACUCCUUCAG	375	6755	CUGAAAAGGAUGGUCUGUU	802
6751	GAGUUUCUGAGAUUAUGUA	376	6751	GAGUUUCUGAGAUUAUGUA	376	6773	UACAUUAUCUCAGAAACUC	803
6769	ACGUGGAACAGUCUGGGUG	377	6769	ACGUGGAACAGUCUGGGUG	377	6791	CACCCAGACUGUUCACCGU	804
6787	GGAAUGGGGCUGAAACCAU	378	6787	GGAAUGGGGCUGAAACCAU	378	6809	AUGGUUUACAGCCCCAUUCC	805
6805	UGUGCAAGUCUGUCUUG	379	6805	UGUGCAAGUCUGUCUUG	379	6827	CAAGACACAGACUUGCACA	806
6823	GUCAGUCCAAGAAGUGACA	380	6823	GUCAGUCCAAGAAGUGACA	380	6845	UGUCACUUCUUGGACUGAC	807
6841	ACCGAGAUUUUAUUUAAG	381	6841	ACCGAGAUUUUAUUUAAG	381	6863	CUAAAAUUAACAUCUCGGU	808
6859	GGGACCCGUGCCUUGUUUC	382	6859	GGGACCCGUGCCUUGUUUC	382	6881	GAAACAAGGCACGGGUCCC	809
6877	CCUAGCCCACAAGAAUGCA	383	6877	CCUAGCCCACAAGAAUGCA	383	6899	UGCAUUCUUGUGGGGUJAGG	810
6895	AAACAUCAAACAGAUACUC	384	6895	AAACAUCAAACAGAUACUC	384	6917	GAGUAUCUGUUUGAUUUU	811
6913	CGCUAGCCCUAUUUAAUU	385	6913	CGCUAGCCCUAUUUAAUU	385	6935	AAUUAAAAUGAGGCUAGCG	812
6931	UGAUUAAAGGAGAGUGCA	386	6931	UGAUUAAAGGAGAGUGCA	386	6953	UGCACUCCUCCUUUUAUCA	813
6949	AUCUUUGGCCGACAGUGGU	387	6949	AUCUUUGGCCGACAGUGGU	387	6971	ACCACUGUCGGCCAAAGAU	814
6967	UGUAACUGUGUGUGUGUGU	388	6967	UGUAACUGUGUGUGUGUGU	388	6989	ACACACACACACAGUUACA	815
6985	UGUGUGUGUGUGUGUGUGU	389	6985	UGUGUGUGUGUGUGUGUGU	389	7007	ACACACACACACACACA	816
7003	UGUGUGUGUGUGGGUGUGG	390	7003	UGUGUGUGUGUGGGUGUGG	390	7025	CCACACCCACACACACA	817

7021	GGUGUAUGUGUUUUUGUG	391	7021	GGUGUAUGUGUUUUUGUG	391	7043	CACAAAAACACAUACACC	818
7039	GCAUAAACUAAUUAAAGGAAA	392	7039	GCAUAAACUAAUUAAAGGAAA	392	7061	UUUCCUUAAAUAGUUUAGC	819
7057	ACUGGAAUUUUAAAGUUUAC	393	7057	ACUGGAAUUUUAAAGUUUAC	393	7079	GUAACUUUUAAAAUCCAGU	820
7075	CUUUUAUACAAACCAGAA	394	7075	CUUUUAUACAAACCAGAA	394	7097	UUCUUGGUUUUAUAAAAAG	821
7093	AUAUAUGCUACAGAUUAA	395	7093	AUAUAUGCUACAGAUUAA	395	7115	UUAUAUCUGUAGCAUUAU	822
7111	AGACAGACAUGGUUUUGGUC	396	7111	AGACAGACAUGGUUUUGGUC	396	7133	GACCAAAACCAUGUCUGUCU	823
7129	CCUAUAAUUCUAGUCAUGA	397	7129	CCUAUAAUUCUAGUCAUGA	397	7151	UCAUGACUAGAAAUUAGG	824
7147	AUGAAUGAAUUUUGUAUAC	398	7147	AUGAAUGAAUUUUGUAUAC	398	7169	GUUAACAAAUAUACAUCAU	825
7165	CCAUCUUCAUAAUAUAC	399	7165	CCAUCUUCAUAAUAUAC	399	7187	GUUAUAUAUAUGAAGUAGG	826
7183	CUUAAAAUAUUUCUUAU	400	7183	CUUAAAAUAUUUCUUAU	400	7205	AUUAAGAAAAUUAUUUAAG	827
7201	UUGGGAUUUGUAUUCGUAC	401	7201	UUGGGAUUUGUAUUCGUAC	401	7223	GUACGAUUACAAUCCCAA	828
7219	CCAACUUAUUGAUAAACU	402	7219	CCAACUUAUUGAUAAACU	402	7241	AGUUUAUCAAUUAAAGUUGG	829
7237	UUGGCAACUCUUUUAUGU	403	7237	UUGGCAACUCUUUUAUGU	403	7259	ACAUAAAGCGAUUGCCAA	830
7255	UUCUGUCUCCUCCAUAAA	404	7255	UUCUGUCUCCUCCAUAAA	404	7277	UUUAUGGAAGGAGACAGAA	831
7273	AUUUUUCAAUAUUAUU	405	7273	AUUUUUCAAUAUUAUU	405	7295	AAUAAGUAUUUUUGAAAAU	832
7291	UCAACAAAGAAAGCUCU	406	7291	UCAACAAAGAAAGCUCU	406	7313	AGAGCUUUUUUCUUUGUUA	833
7309	UUUUUUUCCUAAAAUAAA	407	7309	UUUUUUUCCUAAAAUAAA	407	7331	UUUAUUUAGGAAAAAAA	834
7327	ACUCAAUUUAUCCUUGUU	408	7327	ACUCAAUUUAUCCUUGUU	408	7349	ACAAGGAUAAAUUUGAGU	835
7345	UUAGAGCAGAGAAAAUUA	409	7345	UUAGAGCAGAGAAAAUUA	409	7367	UAUUUUUCUCUGCUCUAA	836
7363	AAGAAAAACUUUGAAUUGG	410	7363	AAGAAAAACUUUGAAUUGG	410	7385	CCAUIUCAAAGUUUUUCUU	837
7381	GUCUCAAAAAAUJGCUAAA	411	7381	GUCUCAAAAAAUJGCUAAA	411	7403	UUUJAGCAUUUUUUGAGAC	838
7399	AUAUUUCAAUGGAAACU	412	7399	AUAUUUCAAUGGAAACU	412	7421	AGUUUUCCAUGAAAAUUA	839
7417	UAAUUGUUAAGUUUAGCUGA	413	7417	UAAUUGUUAAGUUUAGCUGA	413	7439	UCAGCUAAACUAAACAUUUA	840
7435	AUUGUAUGGGUUUUCGAA	414	7435	AUUGUAUGGGUUUUCGAA	414	7457	UUCGAAAAACCCCAUACAAU	841
7453	ACCUUUCACUUUUUUGUUUG	415	7453	ACCUUUCACUUUUUUGUUUG	415	7475	CAACAAAAAGUGAAAGGU	842
7471	GUUUUACCUAAUUUCACAAAC	416	7471	GUUUUACCUAAUUUCACAAAC	416	7493	GUUGUGAAAUAGGUAAAAAC	843
7489	CUGUGUAAAUUGCCAAUAA	417	7489	CUGUGUAAAUUGCCAAUAA	417	7511	UUUAUUGGCAAUUUACACAG	844
7507	AUUCUGUCCAUAGAAAAUG	418	7507	AUUCUGUCCAUAGAAAAUG	418	7529	CAUUUJCAUGGACAGGAUU	845
7525	GCAAAUUAUCCAGUGUAGA	419	7525	GCAAAUUAUCCAGUGUAGA	419	7547	UCUACACUGGAUAAUJUGC	846
7543	AUAUAUUUGACCAUACACC	420	7543	AUAUAUUUGACCAUACACC	420	7565	GGUGAUGGUCAAAAUUAU	847
7561	CUAUGGAUAUUGGCUAGUU	421	7561	CUAUGGAUAUUGGCUAGUU	421	7583	AACUAGCCAAUUAUCCAUAG	848
7579	UUUGCCUUUAUUAAGCAAA	422	7579	UUUGCCUUUAUUAAGCAAA	422	7601	UUUGCUUAAUAAAGGCAAA	849
7597	AUUCAUUUUCCAGCCUGAAUG	423	7597	AUUCAUUUUCCAGCCUGAAUG	423	7619	CAUUCAGGCUGAAAUAAU	850
7615	GUCUGCCUUAUAUUAUCUCU	424	7615	GUCUGCCUUAUAUUAUCUCU	424	7637	AGAGAAUAUAUAGGCAGAC	851
7633	UGCUCUUUGUAUUCUCCUU	425	7633	UGCUCUUUGUAUUCUCCUU	425	7655	AAGGAGAAUAACAAAGAGCA	852
7651	UUGAACCCCGUUAACAAUC	426	7651	UUGAACCCCGUUAACAAUC	426	7673	GAUGUUUUUAACGGGUUCAA	853

7662	AAAACAUCUUGGACACUC	427	7662	AAAACAUCUUGGACACUC	427	7684	GAGUGCCACAGGAUGUUUU	854
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VEGFR2 gi|11321596|ref|NM_002253.1

Pos	Target Sequence	Seq ID	UPos	Upper seq	Seq ID	LPos	Lower seq	Seq ID
1	ACUGAGUCCCGGACCCCG	855	1	ACUGAGUCCCGGACCCCG	855	23	CGGGGUCCCGGACUCAGU	1179
19	GGGAGAGCGGUCAGUGUGU	856	19	GGGAGAGCGGUCAGUGUGU	856	41	ACACACUGACCGCUCUCCC	1180
37	UGGUCGCUUGCGUUUCCUCU	857	37	UGGUCGCUUGCGUUUCCUCU	857	59	AGAGGAAACGCAGCGACCA	1181
55	UGCCUGCGCGGGCAUCAC	858	55	UGCCUGCGCGGGCAUCAC	858	77	GUGAUGCCCGCGCAGGCA	1182
73	CUUGCGCGCGCAGAAAGU	859	73	CUUGCGCGCGCAGAAAGU	859	95	ACUUUCUGCGGCGCGCAAG	1183
91	UCCGUCUGGCAGCCUGGAU	860	91	UCCGUCUGGCAGCCUGGAU	860	113	AUCCAGGCUGCCAGACGGA	1184
109	UAUCCUCUCCUACCGGCAC	861	109	UAUCCUCUCCUACCGGCAC	861	131	GUGCCGUAGGAGAGGAUA	1185
127	CCCGCAGACGCCCGUGCAG	862	127	CCCGCAGACGCCCGUGCAG	862	149	CUGCAGGGCGUCUGCGGG	1186
145	GCCGCGGUCGGCGCCCGG	863	145	GCCGCGGUCGGCGCCCGG	863	167	CCGGCGCCGACCGGCGGC	1187
163	GGCUCUCCUAGCCUUGUGC	864	163	GGCUCUCCUAGCCUUGUGC	864	185	CGCACAGGCUAGGGAGCC	1188
181	GCUCAACUGUCCUGCGCUG	865	181	GCUCAACUGUCCUGCGCUG	865	203	CAGCGAGGACAGUUGAGC	1189
199	GCGGGUGCGCGAGUUCC	866	199	GCGGGUGCGCGAGUUCC	866	221	GGAACUCGCGGACCCCGC	1190
217	CACUCCGCGCCUCCUUCU	867	217	CACUCCGCGCCUCCUUCU	867	239	AGAAGGAGGCGGAGGUG	1191
235	UCUAGACAGGCGUGGGAG	868	235	UCUAGACAGGCGUGGGAG	868	257	CUCCAGCGCCUGUCUAGA	1192
253	GAAGAACCAGCUCUCCGAG	869	253	GAAGAACCAGCUCUCCGAG	869	275	CUCGGAGCCGGUUCUUUC	1193
271	GUUCUGGGCAUUUCGCCCG	870	271	GUUCUGGGCAUUUCGCCCG	870	293	CGGGCGAAUUGCCAGAAC	1194
289	GGCUCGAGGUGCAGGAUGC	871	289	GGCUCGAGGUGCAGGAUGC	871	311	GCAUCCUGACCCUCGAGCC	1195
307	CAGAGCAAGUGCUCUGG	872	307	CAGAGCAAGUGCUCUGG	872	329	CCAGCAGCACCUUGCUCUG	1196
325	GCCGUCGCCUUGGCUUCU	873	325	GCCGUCGCCUUGGCUUCU	873	347	AGAGCCACAGGGCGACGGC	1197
343	UGCGUGGAGACCCGGGCCG	874	343	UGCGUGGAGACCCGGGCCG	874	365	CGGCCCCGUGUCCACGCA	1198
361	GCCUCUGUGGGUUUGCCUA	875	361	GCCUCUGUGGGUUUGCCUA	875	383	UAGGCAAAACCCACAGAGGC	1199
379	AGUUUUCUCUUGAUCUGC	876	379	AGUUUUCUCUUGAUCUGC	876	401	GCAGAUCAAGAGAAACACU	1200
397	CCCAGGCUACAGCAUACAA	877	397	CCCAGGCUACAGCAUACAA	877	419	UUUGUAUGCUGAGCCUGGG	1201
415	AAAGACAUACUUAACAUUA	878	415	AAAGACAUACUUAACAUUA	878	437	UAAUUGUAAGUAUGCUUU	1202
433	AAGGCUAAUACAACUCUUC	879	433	AAGGCUAAUACAACUCUUC	879	455	GAAGAGUUUGUAUAGCCUU	1203
451	CAAAUACUUGCAGGGGAC	880	451	CAAAUACUUGCAGGGGAC	880	473	GUCCCCUGCAAGUAUUUG	1204
469	CAGAGGGACUUGGACUGGC	881	469	CAGAGGGACUUGGACUGGC	881	491	GCCAGUCCAAAGUCCUCUG	1205
487	CUUUGGCCCAAAUAAUCAGA	882	487	CUUUGGCCCAAAUAAUCAGA	882	509	UCUGAUUAUUGGGCCAAAG	1206

505	AGUGGCAGUGAGCAAAAGGG	883	505	AGUGGCAGUGAGCAAAAGGG	883	527	CCCUIUGCUCACUGCCACU	1207
523	GUGGAGGUGACUGAGUGCA	884	523	GUGGAGGUGACUGAGUGCA	884	545	UGCACUCAGUCACCUCCAC	1208
541	AGCGAUGGCCUCUUCUGUA	885	541	AGCGAUGGCCUCUUCUGUA	885	563	UACAGAAAGAGGCCAUCGCU	1209
559	AAGACACUCACAAUUCCAA	886	559	AAGACACUCACAAUUCCAA	886	581	UUGGAAUUGUGAGUGUCUU	1210
577	AAAGUGAUCGGAAUUGACA	887	577	AAAGUGAUCGGAAUUGACA	887	599	UGUCAUUUCCGAUCACUUU	1211
595	ACUGGAGCCUACAAGUGCU	888	595	ACUGGAGCCUACAAGUGCU	888	617	AGCACUUUGAGGCUCCAGU	1212
613	UUCUACCGGAAACUGACU	889	613	UUCUACCGGAAACUGACU	889	635	AGUCAGUUUCCCGGUAGAA	1213
631	UUGGCCUCGGUCAUUUAUG	890	631	UUGGCCUCGGUCAUUUAUG	890	653	CAUAAAUGACCGAGGCCAA	1214
649	GUCUAUGUUAAGAUAUACA	891	649	GUCUAUGUUAAGAUAUACA	891	671	UGUAAUCUUUGAACAUAGAC	1215
667	AGAUUCUCCAUUUUAUUGCUU	892	667	AGAUUCUCCAUUUUAUUGCUU	892	689	AAGCAAUAAAUGGAGAUUU	1216
685	UCUGUUAGUGACCAACAUG	893	685	UCUGUUAGUGACCAACAUG	893	707	CAUGUUGGUCACUAACAGA	1217
703	GGAGUCGUGACAUUACUG	894	703	GGAGUCGUGACAUUACUG	894	725	CAGUAAUGUACACGACUCC	1218
721	GAGAACAAAACAAAACUG	895	721	GAGAACAAAACAAAACUG	895	743	CAGUUUUUUUUUGUUCUC	1219
739	GUGGUAUUCCAUGUCUCG	896	739	GUGGUAUUCCAUGUCUCG	896	761	CGAGACAUGGAUUCACCAC	1220
757	GGGUCCAUUCCAUAUCUCA	897	757	GGGUCCAUUCCAUAUCUCA	897	779	UGAGAUUUUGAAAUUGGACCC	1221
775	AACGUGACAUUUUGUGCAA	898	775	AACGUGACAUUUUGUGCAA	898	797	UUGCAAAGUGACACGUAU	1222
793	AGAUACCCGAAAAAGAGAU	899	793	AGAUACCCGAAAAAGAGAU	899	815	AUCUCUUUCUGGGUAUCU	1223
811	UUUGUUCUUGAGGUAACA	900	811	UUUGUUCUUGAGGUAACA	900	833	UGUUAACCAUCAGGGAACAA	1224
829	AGAAUUUCCUGGGACAGCA	901	829	AGAAUUUCCUGGGACAGCA	901	851	UGCUGUCCCGAGGAAAUUCU	1225
847	AAGAAAGGCUUUAUAUUC	902	847	AAGAAAGGCUUUAUAUUC	902	869	GAAUAGUAAAGCCCUUUCUU	1226
865	CCCAGCUACAUGAUCAGCU	903	865	CCCAGCUACAUGAUCAGCU	903	887	AGCUGAUCUGUAGCUGGG	1227
883	UAUGCUGGCAUGGUCUUCU	904	883	UAUGCUGGCAUGGUCUUCU	904	905	AGAAAGCAUUGCCAGCAUA	1228
901	UGUGAAGCAAAAAUUAUUG	905	901	UGUGAAGCAAAAAUUAUUG	905	923	CAUUAAUUUUUGCUUUCACA	1229
919	GAUGAAAGUUAACCAAGUCUA	906	919	GAUGAAAGUUAACCAAGUCUA	906	941	UAGACUGGUAAACUUUACAUC	1230
937	AUUUAUGUACAUAUUGUCG	907	937	AUUUAUGUACAUAUUGUCG	907	959	CGACAACUAUAGUACAUAUU	1231
955	GUUGUAGGGUAUAGGAUUU	908	955	GUUGUAGGGUAUAGGAUUU	908	977	AAAUCCUAUACCCUACAAC	1232
973	UAUGAUGUGGUUUCUGAGUC	909	973	UAUGAUGUGGUUUCUGAGUC	909	995	GACUCAGAAACCAUCAUAUA	1233
991	CCGUCUCAUGGAUUUGAAC	910	991	CCGUCUCAUGGAUUUGAAC	910	1013	GUUCAUUUCCAUAGAGACGG	1234
1009	CUAUCUGUUGGAGAAAAAGC	911	1009	CUAUCUGUUGGAGAAAAAGC	911	1031	GCUUUUCUCCAAACAGAUAG	1235
1027	CUUGUCUUAAAUGUACAG	912	1027	CUUGUCUUAAAUGUACAG	912	1049	CUGUACAAUUUAAGACAAAG	1236
1045	GCAAGAACUGAACUAAAUG	913	1045	GCAAGAACUGAACUAAAUG	913	1067	CAUUUAGUUUCAGUUUCUUGC	1237
1063	GUGGGAUUAGACUUAACU	914	1063	GUGGGAUUAGACUUAACU	914	1085	AGUUAGAGUGCAUUCUCCAC	1238
1081	UGGGAUAACCCUUCUUCGA	915	1081	UGGGAUAACCCUUCUUCGA	915	1103	UCGAAAGAGGGUAUUCCCA	1239
1099	AAGCAUCAGCAUAAGAAAC	916	1099	AAGCAUCAGCAUAAGAAAC	916	1121	GUUUUUUAUGCUGAUGCUU	1240
1117	CUUGUAAACCGAGACCUAA	917	1117	CUUGUAAACCGAGACCUAA	917	1139	UUAGGUCUCGGUUUUAACAAG	1241
1135	AAAACCCAGUCUGGGAGUG	918	1135	AAAACCCAGUCUGGGAGUG	918	1157	CACUCCAGACUGGGUUUUU	1242

1153	GAGAUGAAGAAAAUUUUUGA	919	1153	GAGAUGAAGAAAAUUUUUGA	919	1175	UAAAAUUUUCUUCUACUC	1243
1171	AGCACCUUAACUUAUAGAUG	920	1171	AGCACCUUAACUUAUAGAUG	920	1193	CAUCUUAAGUUAAGGUCU	1244
1189	GGUGUAACCCGGAGUGACC	921	1189	GGUGUAACCCGGAGUGACC	921	1211	GGUCACUCCGGGUUACACC	1245
1207	CAAGGAUUUGUACACCUGUG	922	1207	CAAGGAUUUGUACACCUGUG	922	1229	CACAGGUGUACAAUCCUUG	1246
1225	GCAGCAUCCAGUGGGCUGA	923	1225	GCAGCAUCCAGUGGGCUGA	923	1247	UCAGCCCACUGGAUGCUGC	1247
1243	AUGACCAAGAAACACAGCA	924	1243	AUGACCAAGAAACACAGCA	924	1265	UGCUGUUUUCUUGGUCAU	1248
1261	ACAUUUGUCAGGUCCAUUG	925	1261	ACAUUUGUCAGGUCCAUUG	925	1283	CAUGGACCCUGACAAUUGU	1249
1279	GA AAAACCUUUUUGUUGCUU	926	1279	GA AAAACCUUUUUGUUGCUU	926	1301	AAGCAACAAAAAGUUUUUC	1250
1297	UUUGGAUGUGGCAUGGAAU	927	1297	UUUGGAUGUGGCAUGGAAU	927	1319	AUUC CAUGCCACUUC CAAA	1251
1315	UCUCUGGGUGAAGCCACGG	928	1315	UCUCUGGGUGAAGCCACGG	928	1337	CCGUGGCUUCCACCAGAGA	1252
1333	GUGGGGAGCGUGUCAGAA	929	1333	GUGGGGAGCGUGUCAGAA	929	1355	UUCUGACACGCUCCCCAC	1253
1351	AUCCUGCGAAGUACCUUG	930	1351	AUCCUGCGAAGUACCUUG	930	1373	CAAGGUACUUCG CAGGGAU	1254
1369	GGUACCCACCCCCAGAAA	931	1369	GGUACCCACCCCCAGAAA	931	1391	UUUCUGGGGUGGGAUACC	1255
1387	AUAAAUGGUUAAAAAUG	932	1387	AUAAAUGGUUAAAAAUG	932	1409	CAUUUUUAUACCAUUUUUAU	1256
1405	GGAUACCCCUUAGAGUCCA	933	1405	GGAUACCCCUUAGAGUCCA	933	1427	UGGACUC AAGGGGU AUUCC	1257
1423	AUACACACAAUUAAGCGG	934	1423	AUACACACAAUUAAGCGG	934	1445	CCGCUUUAUUUGUGAUU	1258
1441	GGGCAUGUACUGACGAUUA	935	1441	GGGCAUGUACUGACGAUUA	935	1463	UAUUGCUCAGUACAUGCC	1259
1459	AUGGAUGUGAGUGAAAGAG	936	1459	AUGGAUGUGAGUGAAAGAG	936	1481	CUCUUACACUCACUUC CAU	1260
1477	GACACAGGAUUUACACUG	937	1477	GACACAGGAUUUACACUG	937	1499	CAGUGUAAUUUCCUGUGUC	1261
1495	GUCAUCCUUAACCAUCCCA	938	1495	GUCAUCCUUAACCAUCCCA	938	1517	UGGGAUUGGU AAGGAUGAC	1262
1513	AUUCAAAGGAGAGAGCAGA	939	1513	AUUCAAAGGAGAGAGCAGA	939	1535	UCUGCUUCCU UUGAAAU	1263
1531	AGCAUGUGGUCUCUCUGG	940	1531	AGCAUGUGGUCUCUCUGG	940	1553	CCAGAGAGACCAUUGGCU	1264
1549	GUUGUGUAUGUCCACCCC	941	1549	GUUGUGUAUGUCCACCCC	941	1571	GGGGUGGGACAUACACAAC	1265
1567	CAGAUUGGUGAGAAUUCUC	942	1567	CAGAUUGGUGAGAAUUCUC	942	1589	GAGAUUUCUCACCAAUUCUG	1266
1585	CUAAUCUCUCUGUGGAUU	943	1585	CUAAUCUCUCUGUGGAUU	943	1607	AAUCCACAGAGAGAUUAG	1267
1603	UCCUACAGUACGGCACCA	944	1603	UCCUACAGUACGGCACCA	944	1625	UGGUGCCGUACUGGUAGGA	1268
1621	ACUCAACGCGUACAU GUA	945	1621	ACUCAACGCGUACAU GUA	945	1643	UACAUGUCAGCGUUUGAGU	1269
1639	ACGGUCUAUGCCAUUCCUC	946	1639	ACGGUCUAUGCCAUUCCUC	946	1661	GAGGAUUGGCAUAGACCGU	1270
1657	CCCCCGCAUCACAUCCACU	947	1657	CCCCCGCAUCACAUCCACU	947	1679	AGUGGAUGUGAU GCGGGGG	1271
1675	UGGUUUUGGAGUUUGGAGG	948	1675	UGGUUUUGGAGUUUGGAGG	948	1697	CCUCCAAACUGCCAAUACCA	1272
1693	GAAGAGUGCGCCAAACGAGC	949	1693	GAAGAGUGCGCCAAACGAGC	949	1715	GCUCGUUUGGCGCACUCUUC	1273
1711	CCAGCCAAAGCUGUCUCAG	950	1711	CCAGCCAAAGCUGUCUCAG	950	1733	CUGAGACAGCUUGGCU GGG	1274
1729	GUGACAAAACCAUACCCU	951	1729	GUGACAAAACCAUACCCU	951	1751	AAGGUAUUGGGUUUGUCAC	1275
1747	UGUGAAGAAUGGAGAAGUG	952	1747	UGUGAAGAAUGGAGAAGUG	952	1769	CACUUCUCCAUUCUUCACA	1276
1765	GUGGAGGACUUC CAGGGAG	953	1765	GUGGAGGACUUC CAGGGAG	953	1787	CUCCUGGAAAGUCCUGCAC	1277
1783	GGAAUUAUUUUUGAAGUUA	954	1783	GGAAUUAUUUUUGAAGUUA	954	1805	UAACUUC AAAAAUUUUUCC	1278

1801	AAUAAAAUCAUUUUGCUC	955	1801	AAUAAAAUCAUUUUGCUC	955	1823	GAGCAAAUUGAUUUUUUU	1279
1819	CUAAUUUGAAGGAAAAACA	956	1819	CUAAUUUGAAGGAAAAACA	956	1841	UGUUUUUUCCUUCAAUUAG	1280
1837	AAACUGUAAGUACCCUUG	957	1837	AAAACUGUAAGUACCCUUG	957	1859	CAAGGGUACUACAGUUUU	1281
1855	GUUAUCCAAGCGGCAAAUG	958	1855	GUUAUCCAAGCGGCAAAUG	958	1877	CAUUGCCGCUUGGAUAAC	1282
1873	GUGUCAGCUUUGUACAAAU	959	1873	GUGUCAGCUUUGUACAAAU	959	1895	AUUGUACAAAAGCUGACAC	1283
1891	UGUGAAGCGGUCAACAAAG	960	1891	UGUGAAGCGGUCAACAAAG	960	1913	CUUUGUUGACCGCUUCACA	1284
1909	GUCGGGAGAGGAGAGGGG	961	1909	GUCGGGAGAGGAGAGGGG	961	1931	CCCUCUCUCUCUCCCGAC	1285
1927	GUGAUCUCCUCCACGUGA	962	1927	GUGAUCUCCUCCACGUGA	962	1949	UCACGUGGAAGGAGAUAC	1286
1945	ACCAGGGUCCUGAAAUUA	963	1945	ACCAGGGUCCUGAAAUUA	963	1967	UAAUUUCAGGACCCCGGU	1287
1963	ACUUUGCAACCUGACAUGC	964	1963	ACUUUGCAACCUGACAUGC	964	1985	GCAUGUCAGGUUGCAAAAGU	1288
1981	CAGCCACUGAGCAGGAGA	965	1981	CAGCCACUGAGCAGGAGA	965	2003	UCUCCUGCUCAGUGGGCUG	1289
1999	AGCGUGUCUUUGUGUGCA	966	1999	AGCGUGUCUUUGUGUGCA	966	2021	UGCACCACAAAAGACACGCU	1290
2017	ACUGCAGACAGAUUACGU	967	2017	ACUGCAGACAGAUUACGU	967	2039	ACGUAGAUCUGUCUGCAGU	1291
2035	UUUGAGAACCUCAUAUGGU	968	2035	UUUGAGAACCUCAUAUGGU	968	2057	ACCAUGUGAGGUUCUCUCAA	1292
2053	UACAAGCUUGGCCACACAGC	969	2053	UACAAGCUUGGCCACACAGC	969	2075	GCUGUGGGCCAAGCUUGUA	1293
2071	CCUCUGCCAAUCCAUGUGG	970	2071	CCUCUGCCAAUCCAUGUGG	970	2093	CCCAUGGAUUUGGCAGAGG	1294
2089	GGAGAGUUGCCACACACUUG	971	2089	GGAGAGUUGCCACACUUG	971	2111	CAGUGUGGGCAACUCUCC	1295
2107	GUUUGCAAGAACUUGGAUA	972	2107	GUUUGCAAGAACUUGGAUA	972	2129	UAUCCAAUUCUUGCAAAC	1296
2125	ACUCUUUGGAAAUUGAAUG	973	2125	ACUCUUUGGAAAUUGAAUG	973	2147	CAUUCAAUUUCCAAGAGU	1297
2143	GCCACCAUGUUCUCUAAUA	974	2143	GCCACCAUGUUCUCUAAUA	974	2165	UAUAGAGAACAUGUGGC	1298
2161	AGCACAAUAGACAUUUUGA	975	2161	AGCACAAUAGACAUUUUGA	975	2183	UCAAAAUGUACAUUUGGCU	1299
2179	AUCAUGGAGCUUAAAGAAUG	976	2179	AUCAUGGAGCUUAAAGAAUG	976	2201	CAUUCUUAAAGCUCCAUGAU	1300
2197	GCAUCCUUUGCAGGACCAAG	977	2197	GCAUCCUUUGCAGGACCAAG	977	2219	CUUGGUCCUGGCAAGGAUGC	1301
2215	GGAGACUAGUCUGCCUUG	978	2215	GGAGACUAGUCUGCCUUG	978	2237	CAAGGCAGACAUAGUCC	1302
2233	GCUCAAGACAGGAAGACCA	979	2233	GCUCAAGACAGGAAGACCA	979	2255	UGGUCUCCUGUCUUGAGC	1303
2251	AAGAAAAGACAUUUGCGUGG	980	2251	AAGAAAAGACAUUUGCGUGG	980	2273	CCACGCAAUGUCUUUUCU	1304
2269	GUCAGGCAGCUCACAGUCC	981	2269	GUCAGGCAGCUCACAGUCC	981	2291	GGACUGUGAGCUGCCUAG	1305
2287	CUAGAGCGUGUGGCACCCA	982	2287	CUAGAGCGUGUGGCACCCA	982	2309	UGGGUGCCACACGCUUAG	1306
2305	ACGAUCACAGGAACCCUGG	983	2305	ACGAUCACAGGAACCCUGG	983	2327	CCAGGUUCCUGUGAUCGU	1307
2323	GAGAAUCAGACGACAAAGUA	984	2323	GAGAAUCAGACGACAAAGUA	984	2345	UACUUGUCGUCUGAUUCUC	1308
2341	AUUGGGGAAAGCAUCGAAG	985	2341	AUUGGGGAAAGCAUCGAAG	985	2363	CUUCGAUGCUUUCGCCAAU	1309
2359	GUCUCAUGCAGCGCAUCUG	986	2359	GUCUCAUGCAGCGCAUCUG	986	2381	CAGAUCCCGUGCAUGAGAC	1310
2377	GGGAAUCCCCCUCCACAGA	987	2377	GGGAAUCCCCCUCCACAGA	987	2399	UCUGUGGAGGGGGAUUC	1311
2395	AUCAUGUGGUUUAAGAUUA	988	2395	AUCAUGUGGUUUAAGAUUA	988	2417	UAUCUUUAAACCACAUAGAU	1312
2413	AAUGAGACCCUUGUAGAAAG	989	2413	AAUGAGACCCUUGUAGAAAG	989	2435	CUUCUACAAGGGGCUCAUU	1313
2431	GACUCAGGCAUUUGUAUUGA	990	2431	GACUCAGGCAUUUGUAUUGA	990	2453	UCAAUACAAGCCUGAGUC	1314

2449	AAGGAUGGGAACCGGAACC	991	2449	AAGGAUGGGAACCGGAACC	991	2471	GGUCCGGUUCUCCAUCCUU	1315
2467	CUCACUAUCCGCAGAGUGA	992	2467	CUCACUAUCCGCAGAGUGA	992	2489	UCACUCUGCGGAUAGUGAG	1316
2485	AGGAAGGAGGACGAAGGCC	993	2485	AGGAAGGAGGACGAAGGCC	993	2507	GGCCUUCUGUCCUCCUCCU	1317
2503	CUCUACACCUUGCCAGGCAU	994	2503	CUCUACACCUUGCCAGGCAU	994	2525	AUGCCUGGCAGGUGUAGAG	1318
2521	UGCAGUUGUUCUUGGCUGUG	995	2521	UGCAGUUGUUCUUGGCUGUG	995	2543	CACAGCCAAGAACACUJGCA	1319
2539	GCAAAAGUGGAGGCAUUUU	996	2539	GCAAAAGUGGAGGCAUUUU	996	2561	AAAAUGCCUCCACUUIUUGC	1320
2557	UUCAUAUAAGAGGUGCCC	997	2557	UUCAUAUAAGAGGUGCCC	997	2579	GGGCACCUUCUAUUAUGAA	1321
2575	CAGGAAAAGACGAACUUGG	998	2575	CAGGAAAAGACGAACUUGG	998	2597	CCAAUUCUGUCUUUCCUG	1322
2593	GAUAUCAUAUUCUAGUAG	999	2593	GAUAUCAUAUUCUAGUAG	999	2615	CUACUAGAAUAUUAUUAUC	1323
2611	GGCACGGCGGUGAUUGCCA	1000	2611	GGCACGGCGGUGAUUGCCA	1000	2633	UGGCAAUACCCGCCGUGCC	1324
2629	AUGUUCUUGGCUACUUC	1001	2629	AUGUUCUUGGCUACUUC	1001	2651	GAAGUAGCCAGAAGAACAUC	1325
2647	CUUGUCAUCCUACCGGA	1002	2647	CUUGUCAUCCUACCGGA	1002	2669	UCCGUAGGAUGAUGACAAG	1326
2665	ACCGUUAAGCGGGCCAAUG	1003	2665	ACCGUUAAGCGGGCCAAUG	1003	2687	CAUUGGCCCGCUUAACGGU	1327
2683	GGAGGGAAACUGAAGACAG	1004	2683	GGAGGGAAACUGAAGACAG	1004	2705	CUGUCUUCAGUUCGCCUCC	1328
2701	GGCUACUUGUCCAUUCGUA	1005	2701	GGCUACUUGUCCAUUCGUA	1005	2723	UGACGAUGGACAAGUAGCC	1329
2719	AUGGAUCCAGAUAAUCC	1006	2719	AUGGAUCCAGAUAAUCC	1006	2741	GGAGUUAUCUGGAUCCAU	1330
2737	CCAUUGGAUGAACAUUGUG	1007	2737	CCAUUGGAUGAACAUUGUG	1007	2759	CACAAUUAUUAUCCAAUGG	1331
2755	GAACGACUGCCUUAUGAUG	1008	2755	GAACGACUGCCUUAUGAUG	1008	2777	CAUCAUAAGGCAUGUUC	1332
2773	GCCAGCAAUUGGGAUUC	1009	2773	GCCAGCAAUUGGGAUUC	1009	2795	GGAAUJCCCAUJUUGCUGGC	1333
2791	CCCAGAGACCGGCUAAGC	1010	2791	CCCAGAGACCGGCUAAGC	1010	2813	GCUUCAGCCGGUCUCUGGG	1334
2809	CUAGGUAAGCCUUCUUGGCC	1011	2809	CUAGGUAAGCCUUCUUGGCC	1011	2831	GGCCAAGAGGCUUJACCUG	1335
2827	CGUGGUGCCUUUGGCCAAG	1012	2827	CGUGGUGCCUUUGGCCAAG	1012	2849	CUUGGCCAAAGGCCACCAG	1336
2845	GUGAUUGAAGCAGAUGCCU	1013	2845	GUGAUUGAAGCAGAUGCCU	1013	2867	AGGCAUCUGCUUCAUUCAC	1337
2863	UUUGGAAUUGACAAGACAG	1014	2863	UUUGGAAUUGACAAGACAG	1014	2885	CUGUCUUGUCAAUUCCAAA	1338
2881	GCAACUUGCAGGACAGUAG	1015	2881	GCAACUUGCAGGACAGUAG	1015	2903	CUACUGUCCUGCAAGUUGC	1339
2899	GCAGUCAAAUUGUUGAAAG	1016	2899	GCAGUCAAAUUGUUGAAAG	1016	2921	CUUUAACAUAUUUUGACUUC	1340
2917	GAAGGAGCAACACACAGUG	1017	2917	GAAGGAGCAACACACAGUG	1017	2939	CACUGUGUGUUGCUCUUC	1341
2935	GAGCAUCGAGCUCUCAUGU	1018	2935	GAGCAUCGAGCUCUCAUGU	1018	2957	ACAUGAGAGCUCGAUGCUC	1342
2953	UCUGAACUCAAGAUCCUCA	1019	2953	UCUGAACUCAAGAUCCUCA	1019	2975	UGAGGAUCUUGAGUUCAGA	1343
2971	AUUCAUUAUUGGUACCAUC	1020	2971	AUUCAUUAUUGGUACCAUC	1020	2993	GAUGGUGACCACAAUUGAAU	1344
2989	CUCAAUUGUGUACACCUUC	1021	2989	CUCAAUUGUGUACACCUUC	1021	3011	GAAGGUUGACCACAAUUGAG	1345
3007	CUAGGUGCCUUGUACCAAGC	1022	3007	CUAGGUGCCUUGUACCAAGC	1022	3029	GCUUGGUACAGGCACCUAG	1346
3025	CCAGGAGGGCCACUCAUGG	1023	3025	CCAGGAGGGCCACUCAUGG	1023	3047	CCAUGAGUGGCCUCCUGG	1347
3043	GUGAUUGUGGAAUUCUGCA	1024	3043	GUGAUUGUGGAAUUCUGCA	1024	3065	UGCAGAAUUCACAAUUCAG	1348
3061	AAAUUUGGAAACCUGUCCA	1025	3061	AAAUUUGGAAACCUGUCCA	1025	3083	UGGACAGGUUUCCAAUUU	1349
3079	ACUUACCUAGAGGAGCAAGA	1026	3079	ACUUACCUAGAGGAGCAAGA	1026	3101	UCUUGCUCCUCAGGUAAAGU	1350

3097	AGAAUUGAAUUUGUCCCCU	1027	3097	AGAAUUGAAUUUGUCCCCU	1027	3119	AGGGACAAAUUCAUUUCU	1351
3115	UACAAGACCAAAAGGGGCAC	1028	3115	UACAAGACCAAAAGGGGCAC	1028	3137	GUGCCCCUUGGUCUUGUA	1352
3133	CGAUUCCGUCAAGGGAAG	1029	3133	CGAUUCCGUCAAGGGAAG	1029	3155	CUUCCCCUUGACGGAUUCG	1353
3151	GACUACGUUGGAGCAAUCC	1030	3151	GACUACGUUGGAGCAAUCC	1030	3173	GGAUUGCUCCAACGUAGUC	1354
3169	CCUGUGGAUCUGAAACGGC	1031	3169	CCUGUGGAUCUGAAACGGC	1031	3191	GCCGUUUCAGAUCCACAGG	1355
3187	CGCUUGGACAGCAUCACCA	1032	3187	CGCUUGGACAGCAUCACCA	1032	3209	UGGUGAUGCUGUCCAAGCG	1356
3205	AGUAGCCAGAGCUCAGCCA	1033	3205	AGUAGCCAGAGCUCAGCCA	1033	3227	UGGCUAGCUCUGGCUACU	1357
3223	AGCUCUGGAUUUGUGGAGG	1034	3223	AGCUCUGGAUUUGUGGAGG	1034	3245	CCUCCACAAAUCCAGAGCU	1358
3241	GAGAAGUCCUCAGUGAUG	1035	3241	GAGAAGUCCUCAGUGAUG	1035	3263	CAUCACUGAGGGACUUCUC	1359
3259	GUAGAAGAAGGAAGCUC	1036	3259	GUAGAAGAAGGAAGCUC	1036	3281	GAGCUUCCUUCUUCUAC	1360
3277	CCUGAAGAUUCGUUAAGG	1037	3277	CCUGAAGAUUCGUUAAGG	1037	3299	CCUUAUACAGAUUCUACAGG	1361
3295	GACUCCUGACCUUGGAGC	1038	3295	GACUCCUGACCUUGGAGC	1038	3317	GCUCCAAGGUCAGGAAGUC	1362
3313	CAUCUCAUCUGUACAGCU	1039	3313	CAUCUCAUCUGUACAGCU	1039	3335	AGCUGUAACAGAUAGAGUG	1363
3331	UCCCAAGUGGCUAAGGGCA	1040	3331	UCCCAAGUGGCUAAGGGCA	1040	3353	UGCCCUUAGCCACUUGGAA	1364
3349	AUGGAGUUCUUGGCAUCGC	1041	3349	AUGGAGUUCUUGGCAUCGC	1041	3371	GCGAUGCCAAAGAACUCCAU	1365
3367	CGAAAGUGUAUCCACAGGG	1042	3367	CGAAAGUGUAUCCACAGGG	1042	3389	CCUGUGGAUACACUUCUG	1366
3385	GACCUGGCGGCACGAAUA	1043	3385	GACCUGGCGGCACGAAUA	1043	3407	UAUUUCGUGCCGCCAGGUC	1367
3403	AUCCUCUUAUCGGAGAAGA	1044	3403	AUCCUCUUAUCGGAGAAGA	1044	3425	UCUUCUCCGAUAAAGAGAU	1368
3421	AACGUGGUUAAAUUCUGUG	1045	3421	AACGUGGUUAAAUUCUGUG	1045	3443	CACAGUUUUAAACACGUAU	1369
3439	GACUUUGGCUUGGCCCGGG	1046	3439	GACUUUGGCUUGGCCCGGG	1046	3461	CCGGGCCAAAGCCAAAGUC	1370
3457	GAUUAUUUAUAAAGAUCCAG	1047	3457	GAUUAUUUAUAAAGAUCCAG	1047	3479	CUGGAUCUUAUAAAUUUC	1371
3475	GAUUAUGUCAGAAAAGGAG	1048	3475	GAUUAUGUCAGAAAAGGAG	1048	3497	CUCCUUUUCUGACAUAAUC	1372
3493	GAUGCUCGCCUCCCUUUGA	1049	3493	GAUGCUCGCCUCCCUUUGA	1049	3515	UCAAAGGGAGGCGAGCAUC	1373
3511	AAUUGAUGGCCCCAGAAA	1050	3511	AAUUGAUGGCCCCAGAAA	1050	3533	UUUCUGGGCCAUCCAUUU	1374
3529	ACAAUUUUUGACAGAGUGU	1051	3529	ACAAUUUUUGACAGAGUGU	1051	3551	ACACUCUGUCAAAAAUUGU	1375
3547	UACACAAUCCAGAGUGACG	1052	3547	UACACAAUCCAGAGUGACG	1052	3569	CGUCACUCUGGAUUUGUGUA	1376
3565	GUCUGGUCUUUUGGUGUUU	1053	3565	GUCUGGUCUUUUGGUGUUU	1053	3587	AAACACCAAAAGACCAGAC	1377
3583	UUGCUGUGGGAAUAUUUU	1054	3583	UUGCUGUGGGAAUAUUUU	1054	3605	AAAAUUUUUCCACAGCAA	1378
3601	UCCUUAAGGUGCUUCUCCAU	1055	3601	UCCUUAAGGUGCUUCUCCAU	1055	3623	AUGGAGAAGCACCUUAGGA	1379
3619	UAUCCUGGGUAAAGAUUG	1056	3619	UAUCCUGGGUAAAGAUUG	1056	3641	CAAUUUUACCCACAGGAUA	1380
3637	GAUGAAGAAUUUUGUAGGC	1057	3637	GAUGAAGAAUUUUGUAGGC	1057	3659	GCCUACAAAAUUUCUUCUAC	1381
3655	CGAUUGAAAGAGGAACUA	1058	3655	CGAUUGAAAGAGGAACUA	1058	3677	UAGUCCUUCUUAUCAAUCG	1382
3673	AGAAUGAGGGCCCUUGAUU	1059	3673	AGAAUGAGGGCCCUUGAUU	1059	3695	AAUCAGGGGCCCUCAUUUCU	1383
3691	UAUACUACACCAGAAUUGU	1060	3691	UAUACUACACCAGAAUUGU	1060	3713	ACAUUUCUGGUGUAGUAUA	1384
3709	UACCAGACCAUGCUGGACU	1061	3709	UACCAGACCAUGCUGGACU	1061	3731	AGUCCAGCAUGGUCUGGUA	1385
3727	UGCUGGCACGGGGAGCCCA	1062	3727	UGCUGGCACGGGGAGCCCA	1062	3749	UGGCUUCCCCGUGCCAGCA	1386

3745	AGUCAGAGACCCACGUAUUU	1063	3745	AGUCAGAGACCCACGUAUUU	1063	3767	AAAACGUGGGUCUCUGACU	1387
3763	UCAGAGUUGGUGGAACAUAU	1064	3763	UCAGAGUUGGUGGAACAUAU	1064	3785	AAGUUCCACCAACUCUGA	1388
3781	UUGGAAAUUCUUGCAAG	1065	3781	UUGGAAAUUCUUGCAAG	1065	3803	CUUGCAAGAGAUUCCCAA	1389
3799	GCUAAUGCUCAGCAGGAUG	1066	3799	GCUAAUGCUCAGCAGGAUG	1066	3821	CAUCCUGCUGAGCAUAGC	1390
3817	GGCAAAGACUACAUUGUUC	1067	3817	GGCAAAGACUACAUUGUUC	1067	3839	GAACAAUGUAGUCUUGCC	1391
3835	CUUCCGAUAUCAGAGACUU	1068	3835	CUUCCGAUAUCAGAGACUU	1068	3857	AAGUCUCUGAUUCGGAAG	1392
3853	UUGAGCAUGGAAGAGGAUU	1069	3853	UUGAGCAUGGAAGAGGAUU	1069	3875	AAUCCUUCUCCAUUCUCAA	1393
3871	UCUGGACUCUCUGCCUA	1070	3871	UCUGGACUCUCUGCCUA	1070	3893	UAGGCAGAGAGUCCAGA	1394
3889	ACCUCACCCUGUUUCCUGUA	1071	3889	ACCUCACCCUGUUUCCUGUA	1071	3911	UACAGGAAACAGGUGAGGU	1395
3907	AUGGAGGAGGAGGAAGUAU	1072	3907	AUGGAGGAGGAGGAAGUAU	1072	3929	AUACUUCUCCUCCUCCAU	1396
3925	UGUGACCCCAAUUCCAUU	1073	3925	UGUGACCCCAAUUCCAUU	1073	3947	AAUGGAAUUGGGGUCACA	1397
3943	UAUGACAACACAGCAGGAA	1074	3943	UAUGACAACACAGCAGGAA	1074	3965	UUCUCUGUGUUGUCAUA	1398
3961	AUCAGUCAGUUCUGCAGA	1075	3961	AUCAGUCAGUUCUGCAGA	1075	3983	UCUGCAGAUACUGACUGAU	1399
3979	AACAGUAAAGCAAGAGCC	1076	3979	AACAGUAAAGCAAGAGCC	1076	4001	GGCUCUUUCGCUUACUGUU	1400
3997	CGGCCUGUGAGUUA AAAA	1077	3997	CGGCCUGUGAGUUA AAAA	1077	4019	UUUUUACACUCACAGGCCG	1401
4015	ACAUUUGAAGAUUCCCGU	1078	4015	ACAUUUGAAGAUUCCCGU	1078	4037	ACGGGAUAUCUUCAAAUGU	1402
4033	UUAGAAGAACCAGAAGUAA	1079	4033	UUAGAAGAACCAGAAGUAA	1079	4055	UUACUUCUGGUUCUUCUAA	1403
4051	AAAGUAAUCCAGAUAGACA	1080	4051	AAAGUAAUCCAGAUAGACA	1080	4073	UGUCAUCUGGGAUUACUUU	1404
4069	AACAGACGGACAGUGGUA	1081	4069	AACAGACGGACAGUGGUA	1081	4091	UACCACUUGCGUCUGGUU	1405
4087	AUGGUUCUUGCCUCAGAA	1082	4087	AUGGUUCUUGCCUCAGAA	1082	4109	CUUCUGAGGCAAGAACCAU	1406
4105	GAGCUGAAACUUUUGGAAG	1083	4105	GAGCUGAAACUUUUGGAAG	1083	4127	CUUCCAAAGUUUUCAGCUC	1407
4123	GACAGAACCAGAAUUAUCUC	1084	4123	GACAGAACCAGAAUUAUCUC	1084	4145	GAGAUAAUUGGUUCUGUC	1408
4141	CCAUCUUUUGGUGGAUUGG	1085	4141	CCAUCUUUUGGUGGAUUGG	1085	4163	CCAUUCCACCAAAAAGUGG	1409
4159	GUGCCAGCAAAAGCAGGG	1086	4159	GUGCCAGCAAAAGCAGGG	1086	4181	CCUUGCUUUUGCUGGGCAC	1410
4177	GAGUCUGUGGCAUCUGAAG	1087	4177	GAGUCUGUGGCAUCUGAAG	1087	4199	CUUCAGAUGCCACAGACUC	1411
4195	GGCUCAAACAGACAAGCG	1088	4195	GGCUCAAACAGACAAGCG	1088	4217	CGCUUGUCUGGUUUGAGCC	1412
4213	GGCUACCAUCCGGUAUUC	1089	4213	GGCUACCAUCCGGUAUUC	1089	4235	GAUUAUCCGACUGGUAGCC	1413
4231	CACUCCGAUGACACAGACA	1090	4231	CACUCCGAUGACACAGACA	1090	4253	UGUCUGUGUAUCUGGAGUG	1414
4249	ACCACCGUUAUCCAGUG	1091	4249	ACCACCGUUAUCCAGUG	1091	4271	CACUGGAGUAACACGGUGGU	1415
4267	GAGGAAGCAGAAUUAUAA	1092	4267	GAGGAAGCAGAAUUAUAA	1092	4289	UUAAAAUUUCUGCUUCCUC	1416
4285	AAGCUAGUAGAUUUGGAG	1093	4285	AAGCUAGUAGAUUUGGAG	1093	4307	CUCCAAUCUCUAUCAGCUU	1417
4303	GUGCAAAACCGUAGCACAG	1094	4303	GUGCAAAACCGUAGCACAG	1094	4325	CUGUGCUACCCGGUUUGCAC	1418
4321	GCCAGAUUUCAGGCCUG	1095	4321	GCCAGAUUUCAGGCCUG	1095	4343	CAGGCUGGAGAAUCUGGGC	1419
4339	GACUCGGGACCACACUGA	1096	4339	GACUCGGGACCACACUGA	1096	4361	UCAGUGUGGUCCCGAGUC	1420
4357	AGCUCUCCUCCUGUUUAAA	1097	4357	AGCUCUCCUCCUGUUUAAA	1097	4379	UUUAAACAGGAGGAGAGCU	1421
4375	AAGGAAGCAUCCACACCCC	1098	4375	AAGGAAGCAUCCACACCCC	1098	4397	GGGUGUGGGAUGCUUCCUU	1422

4393	CAACUCCCGGACAUCAU	1099	4393	CAACUCCCGGACAUCAU	1099	4415	AUGUGAUGUCCGGGAGUUG	1423
4411	UGAGAGGUCUGCUCAGAUU	1100	4411	UGAGAGGUCUGCUCAGAUU	1100	4433	AAUCUGAGCAGACCUCUCA	1424
4429	UUUGAAGUGUUGUUCUUUC	1101	4429	UUUGAAGUGUUGUUCUUUC	1101	4451	GAAAGAACACACUUCAAA	1425
4447	CCACCAGCAGGAAGUAGCC	1102	4447	CCACCAGCAGGAAGUAGCC	1102	4469	GGCUACUCCUGCUGGUGG	1426
4465	CGCAUUUGAUUUUCAUUUC	1103	4465	CGCAUUUGAUUUUCAUUUC	1103	4487	GAAUUGAAAAUCAAUUGCG	1427
4483	CGCAACAGAAAAAGGACC	1104	4483	CGCAACAGAAAAAGGACC	1104	4505	GGUCCUUUUUCUGUUGUGG	1428
4501	CUCGGACUGCAGGGAGCCA	1105	4501	CUCGGACUGCAGGGAGCCA	1105	4523	UGGCUCCUGCAGUCCGAG	1429
4519	AGUCUUCUAGGCAUAUCCU	1106	4519	AGUCUUCUAGGCAUAUCCU	1106	4541	AGGAUUAUGCCUAGAAGACU	1430
4537	UGGAAGAGGCUUGUGACCC	1107	4537	UGGAAGAGGCUUGUGACCC	1107	4559	GGGUCACAAGCCUUCUCCA	1431
4555	CAAGAAUGUGUCUGUGUCU	1108	4555	CAAGAAUGUGUCUGUGUCU	1108	4577	AGACACAGACACAUUCUUG	1432
4573	UUCUCCCGAGUUGUACCCUG	1109	4573	UUCUCCCGAGUUGUACCCUG	1109	4595	CAGGUCAACACUGGGAGAA	1433
4591	GAUCCUCUUUUUCAUUA	1110	4591	GAUCCUCUUUUUCAUUA	1110	4613	UGAAUGAAAAAGAGGAUC	1434
4609	AUUJAAAAAGCAUUAUUAU	1111	4609	AUUJAAAAAGCAUUAUUAU	1111	4631	AUGAUAAUGCUUUUUUAAU	1435
4627	UGCCCCUGCUGGGGUCUC	1112	4627	UGCCCCUGCUGGGGUCUC	1112	4649	GAGACCCGAGCAGGGGCA	1436
4645	CACCAUGGGUUAAGAACAA	1113	4645	CACCAUGGGUUAAGAACAA	1113	4667	UUUUUUAUAAACCAUUGUG	1437
4663	AAGAGCUUCAAGCAAUUGC	1114	4663	AAGAGCUUCAAGCAAUUGC	1114	4685	GCCAUGCUUUAAGGCUU	1438
4681	CCCCAUCCUCAAGAAAGUA	1115	4681	CCCCAUCCUCAAGAAAGUA	1115	4703	UACUUUUUUAAGGAGUUGGG	1439
4699	AGCAGUACCUUGGGGAGCUG	1116	4699	AGCAGUACCUUGGGGAGCUG	1116	4721	CAGCUCCCGAGGUACUGCU	1440
4717	GACACUUCUGUAAAAACUAG	1117	4717	GACACUUCUGUAAAAACUAG	1117	4739	CUAGUUUUAACAGAAUGUC	1441
4735	GAAGAUAAACAGGCAACG	1118	4735	GAAGAUAAACAGGCAACG	1118	4757	CGUUCCUGGUUUUAUCUUC	1442
4753	GUAGUGUUUCGAGGUGUUG	1119	4753	GUAGUGUUUCGAGGUGUUG	1119	4775	CAACACCUUGAAACACUUC	1443
4771	GAAGAUGGGAAGGAUUUGC	1120	4771	GAAGAUGGGAAGGAUUUGC	1120	4793	GCAAAUCCUUCCCAUUC	1444
4789	CAGGGCUGAGUCUAUCCAA	1121	4789	CAGGGCUGAGUCUAUCCAA	1121	4811	UUGGAUAGACUCAGCCUG	1445
4807	AGAGCUUUUGUUUAGGACG	1122	4807	AGAGCUUUUGUUUAGGACG	1122	4829	CGUCCUAAACAAAGCCUCU	1446
4825	GUGGGUCCCAAGCCAAGCC	1123	4825	GUGGGUCCCAAGCCAAGCC	1123	4847	GGCUUGGCUUGGGACCCAC	1447
4843	CUUAAUGUGGGAUUUCGGA	1124	4843	CUUAAUGUGGGAUUUCGGA	1124	4865	UCCGAAUUCACACAUAAAG	1448
4861	AUUGAUAGAAAGGAAGACU	1125	4861	AUUGAUAGAAAGGAAGACU	1125	4883	AGUCUUCCUUUUUAUCAAU	1449
4879	UAACGUUACCUUGCUUUUG	1126	4879	UAACGUUACCUUGCUUUUG	1126	4901	CCAAAGCAAGGUAAACGUUA	1450
4897	GAGAGUACUGGAGCCUGCA	1127	4897	GAGAGUACUGGAGCCUGCA	1127	4919	UGCAGGGUCCAGUACUCUC	1451
4915	AAUUGCAUUUGUUUUGCUC	1128	4915	AAUUGCAUUUGUUUUGCUC	1128	4937	GAGCAAAACACAAUGCAUUU	1452
4933	CUGGUGAGGUGGGCAUGG	1129	4933	CUGGUGAGGUGGGCAUGG	1129	4955	CCAUGCCACCCUCCACCAG	1453
4951	GGGUCUGUUCUGAAAUUGA	1130	4951	GGGUCUGUUCUGAAAUUGA	1130	4973	UACAUUUUACAGAACAGACCC	1454
4969	AAAGGUUUCAGACGGGGU	1131	4969	AAAGGUUUCAGACGGGGU	1131	4991	AACCCGUCUGAACCCUUU	1455
4987	UUCUGGUUUUAGAAAGGUUG	1132	4987	UUCUGGUUUUAGAAAGGUUG	1132	5009	CAACCUUCUAAAAACAGAA	1456
5005	GCGUGUUCUUCGAGUUGGG	1133	5005	GCGUGUUCUUCGAGUUGGG	1133	5027	CCCAACUCGAAACACACGC	1457
5023	GCUAAAGUAGAGUUCGUUG	1134	5023	GCUAAAGUAGAGUUCGUUG	1134	5045	CAACGAACUCUACUUUAGC	1458

5041	GUGCUGUUUCUGACUCCUA	1135	5041	GUGCUGUUUCUGACUCCUA	1135	5063	UAGGAGUCAGAAACAGCAC	1459
5059	AAUGAGAGUUCUUCUCCAGA	1136	5059	AAUGAGAGUUCUUCUCCAGA	1136	5081	UCUGGAAGGAACUCUCAUU	1460
5077	ACCGUUAGCUGUCUCCUUG	1137	5077	ACCGUUAGCUGUCUCCUUG	1137	5099	CAAGGAGACAGCUAACGGU	1461
5095	GCCAAGCCCCAGGAAGAAA	1138	5095	GCCAAGCCCCAGGAAGAAA	1138	5117	UUUCUCCUGGGGCUUGGC	1462
5113	AAUGAUGCAGCUCUGGCUC	1139	5113	AAUGAUGCAGCUCUGGCUC	1139	5135	GAGCCAGAGCUGCAUCAUU	1463
5131	CCUUGUCUCCAGGCUGAU	1140	5131	CCUUGUCUCCAGGCUGAU	1140	5153	AUCAGCCUGGGAGACAAGG	1464
5149	UCCUUUAUUCAGAAUACCA	1141	5149	UCCUUUAUUCAGAAUACCA	1141	5171	UGGUUUUCUGAAUAAAGGA	1465
5167	ACAAAGAAAGGACAUUCAG	1142	5167	ACAAAGAAAGGACAUUCAG	1142	5189	CUGAAUGUCCUUUCUUUGU	1466
5185	GCUCAAGGCUCUCCUGCCGU	1143	5185	GCUCAAGGCUCUCCUGCCGU	1143	5207	ACGGCAGGGAGCCUUGAGC	1467
5203	UGUUGAAGAGUUCUGACUG	1144	5203	UGUUGAAGAGUUCUGACUG	1144	5225	CAGUCAGAACUCUUCACCA	1468
5221	GCACAAACCAGCUUCUGGU	1145	5221	GCACAAACCAGCUUCUGGU	1145	5243	ACCAGAAGCUGGUUUGUGC	1469
5239	UUUCUUCUGGAAUGAAUAC	1146	5239	UUUCUUCUGGAAUGAAUAC	1146	5261	GUUUUCAUUC CAGAAAGAA	1470
5257	CCCUCAUAUCUGUCCUGAU	1147	5257	CCCUCAUAUCUGUCCUGAU	1147	5279	AUCAGGACAGAUUGAGGG	1471
5275	UGUGAUUAUGUCUGACUG	1148	5275	UGUGAUUAUGUCUGACUG	1148	5297	CAGUCUCAGACAUUAUCACA	1472
5293	GAAUGCGGGAGGUUCAUUG	1149	5293	GAAUGCGGGAGGUUCAUUG	1149	5315	CAUUGAACCCUCCGCAUUC	1473
5311	GUGAAGCUGUGUGUGGUU	1150	5311	GUGAAGCUGUGUGUGGUU	1150	5333	ACACCACACAGCUUUCAC	1474
5329	UCAAAGUUCAGGAAGGAU	1151	5329	UCAAAGUUCAGGAAGGAU	1151	5351	AUCCUUCCUGAAACUUUGA	1475
5347	UUUUACCCUUUUGUUCUUC	1152	5347	UUUUACCCUUUUGUUCUUC	1152	5369	GAAGAACAAAAGGGUAAAA	1476
5365	CCCCUGUCCCCAACCCAC	1153	5365	CCCCUGUCCCCAACCCAC	1153	5387	GUGGUUUGGGACAGGGGG	1477
5383	CUCUCACCCCGCAACCCAU	1154	5383	CUCUCACCCCGCAACCCAU	1154	5405	AUGGUUUGGGGGUGAGAG	1478
5401	UCAGUAAUUUAGUUAUUUG	1155	5401	UCAGUAAUUUAGUUAUUUG	1155	5423	CAAAUAAUUAUUUACUGA	1479
5419	GGCCUCUACUCCAGUAAAC	1156	5419	GGCCUCUACUCCAGUAAAC	1156	5441	GUUUACUGGAGUAGAGGCC	1480
5437	CCUGAUUGGGUUUGUUCAC	1157	5437	CCUGAUUGGGUUUGUUCAC	1157	5459	GUGAACAAACCCCAAUCAGG	1481
5455	CUCUCUGAAUGAUUAUUAG	1158	5455	CUCUCUGAAUGAUUAUUAG	1158	5477	CUAAUAAUUAUUCAGAGAG	1482
5473	GCCAGACUUCAAAAUUUUU	1159	5473	GCCAGACUUCAAAAUUUUU	1159	5495	AAUAAUUUUUGAAGUCUGGC	1483
5491	UUUAUAGCCCAAAUUUAUA	1160	5491	UUUAUAGCCCAAAUUUAUA	1160	5513	UUUAUUUUUGGGGCUAUAUA	1484
5509	ACAUCUAAUUGAUUAUUUA	1161	5509	ACAUCUAAUUGAUUAUUUA	1161	5531	UAAAUAAUACAAUAGAUUG	1485
5527	AGACUUUUUAACAUUAAGAG	1162	5527	AGACUUUUUAACAUUAAGAG	1162	5549	CUCUAUAUUGUUAAAAAGUCU	1486
5545	GCUUUUUCUACUGAUUUUUU	1163	5545	GCUUUUUCUACUGAUUUUUU	1163	5567	AAAAAUCAGUAGAAAAUAGC	1487
5563	UGCCCUUGUUCUGUCCUUU	1164	5563	UGCCCUUGUUCUGUCCUUU	1164	5585	AAAGGACAGAACCAAGGGCA	1488
5581	UUUUUCAA AAAAGAAAAUG	1165	5581	UUUUUCAA AAAAGAAAAUG	1165	5603	CAUUUUCUUUUUUUGAAAAA	1489
5599	GUGUUUUUUGUUUGGUACC	1166	5599	GUGUUUUUUGUUUGGUACC	1166	5621	GGUACCAAAACAAAAACAC	1490
5617	CAUAGUGUGAAUUGCUGGG	1167	5617	CAUAGUGUGAAUUGCUGGG	1167	5639	CCCAGCAUUUCACACUAUG	1491
5635	GAACAAUGACUAUAAGACA	1168	5635	GAACAAUGACUAUAAGACA	1168	5657	UGUCUUAUAGUCAUUGUUC	1492
5653	AUGCUAUGGCACAUUAUU	1169	5653	AUGCUAUGGCACAUUAUU	1169	5675	AAUAUAUUGUGCCAUAGCAU	1493
5671	UUUAUGUCUGUUUAUGUAG	1170	5671	UUUAUGUCUGUUUAUGUAG	1170	5693	CUACAUAACACAGACUAUAA	1494

5689	GAACAAAUUGAAUAUAUU	1171	5689	GAACAAAUUGAAUAUAUU	1171	5711	AAUAUAUAUAUAUUUUC	1495
5707	UAAAGCCUUUAUAUAUAUG	1172	5707	UAAAGCCUUUAUAUAUAUG	1172	5729	CAUUAUAUAUAAGCUUUA	1496
5725	GAACUUUGUAUAUAUCACA	1173	5725	GAACUUUGUAUAUAUCACA	1173	5747	UGUGAAUAGUAACAAAGUUC	1497
5743	AUUUUGUAUCAGUAUAUAUG	1174	5743	AUUUUGUAUCAGUAUAUAUG	1174	5765	CAUAUAUCAGUAACAAAUA	1498
5761	GUAGCAUAACAAAGGUCAU	1175	5761	GUAGCAUAACAAAGGUCAU	1175	5783	AUGACCUUUUGUAUAGCUAC	1499
5779	UAAUGCUUUUCAGCAUAUAUG	1176	5779	UAAUGCUUUUCAGCAUAUAUG	1176	5801	UCAAUUGCUGAAAAGCAUUA	1500
5797	AUGUCAUUUUUAUAUAAGAA	1177	5797	AUGUCAUUUUUAUAUAAGAA	1177	5819	UUCUUUAUAUAUAUAAGACAU	1501
5812	AGAACAUUGAAAAACUUGA	1178	5812	AGAACAUUGAAAAACUUGA	1178	5834	UCAAGUUUUUUAUAUAUUCU	1502

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Pos	Target Sequence	Seq ID	UPos	Upper seq	Seq ID	LPos	Lower seq	Seq ID
1	ACCCACGCGCAGCGGCCGG	1503	1	ACCCACGCGCAGCGGCCGG	1503	23	CCGGCCGCGUGCGCGUGGGU	1750
19	GAGAUGCAGCGGGGCCGG	1504	19	GAGAUGCAGCGGGGCCGG	1504	41	CGGCGCCCCGCGUGCAUCUC	1751
37	GCGCUGUGCCUGCGACUGU	1505	37	GCGCUGUGCCUGCGACUGU	1505	59	ACAGUCGCAGGCACAGCGC	1752
55	UGGCUCUGCCUGGGACUCC	1506	55	UGGCUCUGCCUGGGACUCC	1506	77	GGAGUCCCGAGGAGAGCCA	1753
73	CUGGACGGCCUGGUGAGUG	1507	73	CUGGACGGCCUGGUGAGUG	1507	95	CACUCACCGAGCCGCUCCAG	1754
91	GACUACUCCAUGACCCCCC	1508	91	GACUACUCCAUGACCCCCC	1508	113	GGGGGUAUGGAGUAGUC	1755
109	CCGACCUUGAACAUACACGG	1509	109	CCGACCUUGAACAUACACGG	1509	131	CCGUGAUGUUAAGGUCGG	1756
127	GAGGAGUCACACGUAUCUG	1510	127	GAGGAGUCACACGUAUCUG	1510	149	CGAUGACGUGUGACUCCUC	1757
145	GACACCGGUGACAGCCUGU	1511	145	GACACCGGUGACAGCCUGU	1511	167	ACAGGCUGUCACCGGUGUC	1758
163	UCCAUCUCCUGCAGGGGAC	1512	163	UCCAUCUCCUGCAGGGGAC	1512	185	GUCCCCUGCAGGAGUGGA	1759
181	CAGCACCCUCCGAGUGGG	1513	181	CAGCACCCUCCGAGUGGG	1513	203	CCCACUCGAGGGGUGCUG	1760
199	GCUUGGCCAGGAGCUCAGG	1514	199	GCUUGGCCAGGAGCUCAGG	1514	221	CCUGAGCUCCUGGCCAAGC	1761
217	GAGCGCCAGCCACCGGAG	1515	217	GAGCGCCAGCCACCGGAG	1515	239	CUCGGUGGGCUGGGCGCCUC	1762
235	GACAAGGACAGCGAGGACA	1516	235	GACAAGGACAGCGAGGACA	1516	257	UGUCCUCGUGUCCUUGUC	1763
253	ACGGGGGUGGUGCGGAGACU	1517	253	ACGGGGGUGGUGCGGAGACU	1517	275	AGUCUCGCACCAACCCCGU	1764
271	UGCGAGGGCACAGACGCCA	1518	271	UGCGAGGGCACAGACGCCA	1518	293	UGGCGUCUGUGCCCUUGCA	1765
289	AGGCCUACUGCAAGGUGU	1519	289	AGGCCUACUGCAAGGUGU	1519	311	ACACCUUGCAGUAGGGCCU	1766
307	UUGCUGCUGCACGAGGUAC	1520	307	UUGCUGCUGCACGAGGUAC	1520	329	GUACCUCGUGCAGCAGCAA	1767
325	CAUGCCAAACGACACAGGCA	1521	325	CAUGCCAAACGACACAGGCA	1521	347	UGCCUGUGUCUUGGCAUG	1768
343	AGCUACGUCUGCUACUACA	1522	343	AGCUACGUCUGCUACUACA	1522	365	UGUAGUAGCAGACGUAGCU	1769
361	AAGUACAUAAGGCACGCA	1523	361	AAGUACAUAAGGCACGCA	1523	383	UGCUGCCUUGAUGUACUU	1770

379	AUCGAGGGCACCACGGCCG	1524	379	AUCGAGGGCACCACGGCCG	1524	401	CGCCCGUGGUGCCUCGAU	1771
397	GCCAGCUCUACGUGUUCG	1525	397	GCCAGCUCUACGUGUUCG	1525	419	CGAACACGUAGGAGCUGGC	1772
415	GUGAGAGACUUUGAGCAGC	1526	415	GUGAGAGACUUUGAGCAGC	1526	437	GCUGCUCAAAAGUCUCAC	1773
433	CCAUUCAUCAACAAGCCUG	1527	433	CCAUUCAUCAACAAGCCUG	1527	455	CAGGCUUGUUGAUAAUGG	1774
451	GACACGCUUUGGUCAACA	1528	451	GACACGCUUUGGUCAACA	1528	473	UGUUGACCAAGAGCGUGUC	1775
469	AGGAAGGACGCCAUGUGGG	1529	469	AGGAAGGACGCCAUGUGGG	1529	491	CCCACAUUGCGUCCUCCU	1776
487	GUGCCCUUGUCUGGUGUCCA	1530	487	GUGCCCUUGUCUGGUGUCCA	1530	509	UGACACCAAGACAGGCGAC	1777
505	AUCCCCGGCCUCAAUUGUA	1531	505	AUCCCCGGCCUCAAUUGUA	1531	527	UGACAUUGAGGCCGGGGAU	1778
523	ACGCUUGCGUCGCAAAAGCU	1532	523	ACGCUUGCGUCGCAAAAGCU	1532	545	AGCUUUGCGAGCGCAGCGU	1779
541	UCGGUGCUGUGGCCAGACG	1533	541	UCGGUGCUGUGGCCAGACG	1533	563	CGUCUGGCCACAGCACCCGA	1780
559	GGCAGGAGGUGGUGUGGG	1534	559	GGCAGGAGGUGGUGUGGG	1534	581	CCCACACCAACCUCUCCGCC	1781
577	GAUGACCGGGGGGCAUGC	1535	577	GAUGACCGGGGGGCAUGC	1535	599	GCAUGCCCCCGCGGUAUC	1782
595	CUCGUGUCCACGCCACUGC	1536	595	CUCGUGUCCACGCCACUGC	1536	617	GCAGUGGCGUGGACACGAG	1783
613	CUGACGAUGCCCUGUACC	1537	613	CUGACGAUGCCCUGUACC	1537	635	GGUACAGGGCAUCGUGCAG	1784
631	CUGCAGUGCGAGACCACCU	1538	631	CUGCAGUGCGAGACCACCU	1538	653	AGGUGGUCUCGCACUCGAG	1785
649	UGGGGAGACCAAGGACUUC	1539	649	UGGGGAGACCAAGGACUUC	1539	671	GGAAGUCCUGGUCUCCCA	1786
667	CUUUCCAACCCCUUCCUGG	1540	667	CUUUCCAACCCCUUCCUGG	1540	689	CCAGGAAGGGGUUGGAAAG	1787
685	GUGCACAUACACAGGCAACG	1541	685	GUGCACAUACACAGGCAACG	1541	707	CGUUGCCUGUGAUGUGCAC	1788
703	GAGCUCUAUGACAUCACAG	1542	703	GAGCUCUAUGACAUCACAG	1542	725	GCUGGAUGUCAUAGAGCUC	1789
721	CUGUUGCCCAAGGAUCGC	1543	721	CUGUUGCCCAAGGAUCGC	1543	743	GCGACUUCUUGGGCAACAG	1790
739	CUGGAGCUCUGGUAGGGG	1544	739	CUGGAGCUCUGGUAGGGG	1544	761	CCCCUACCAAGCAGCUCCAG	1791
757	GAGAAGCUGGUCCUCAACU	1545	757	GAGAAGCUGGUCCUCAACU	1545	779	AGUUGAGGACCAGCUUCUC	1792
775	UGCACCGUGUGGGCUGAGU	1546	775	UGCACCGUGUGGGCUGAGU	1546	797	ACUCAGCCCACACGGUGCA	1793
793	UUUAACUCAGGUGUACCU	1547	793	UUUAACUCAGGUGUACCU	1547	815	AGGUGACACCUAGAGUAAA	1794
811	UUUGACUGGGACUACCCAG	1548	811	UUUGACUGGGACUACCCAG	1548	833	CUGGGUAGUCCCAAGUAAA	1795
829	GGGAAGCAGGCAGAGCGGG	1549	829	GGGAAGCAGGCAGAGCGGG	1549	851	CCCGCUCUGCCUGCUUCCC	1796
847	GGUAAGUGGGUGCCCGAGC	1550	847	GGUAAGUGGGUGCCCGAGC	1550	869	GCUCGGGACCCCAUUAAC	1797
865	CGACGCUCCCAACAGACCC	1551	865	CGACGCUCCCAACAGACCC	1551	887	GGGUCUGUUGGAGCGUCG	1798
883	CACACAGAACUCUCCAGCA	1552	883	CACACAGAACUCUCCAGCA	1552	905	UGCUGGAGAGUUCUGUGUG	1799
901	AUCCUGACCAUCCACAACG	1553	901	AUCCUGACCAUCCACAACG	1553	923	CGUUGGGAUGGUCAGGAU	1800
919	GUCAGCCAGCACGACCUGG	1554	919	GUCAGCCAGCACGACCUGG	1554	941	CCAGGUCGUGCUGGCGAG	1801
937	GGCUCGUAUGUGCAAGG	1555	937	GGCUCGUAUGUGCAAGG	1555	959	CCUUGCACACAUCGAGCC	1802
955	GCCAACAACGGCAUCCAGC	1556	955	GCCAACAACGGCAUCCAGC	1556	977	GCUGGAUGCCGUUGUUGGC	1803

973	CGAUUUCGGGAGAGCACCG	1557	973	CGAUUUCGGGAGAGCACCG	1557	995	CGGUGCUCUCCCCGAAUUCG	1804
991	GAGGUCAUUGUGCAUGAAA	1558	991	GAGGUCAUUGUGCAUGAAA	1558	1013	UUUCAUGCACAAUAGACCUC	1805
1009	AUCCCUUUAUCAGCGUCG	1559	1009	AUCCCUUUAUCAGCGUCG	1559	1031	CGACGCUGAUGAAGGGAUU	1806
1027	GAGUGGCUCAAAGACCCA	1560	1027	GAGUGGCUCAAAGACCCA	1560	1049	UGGUGCCUUUUGAGCCACUC	1807
1045	AUCCUGGAGGCCACGGCAG	1561	1045	AUCCUGGAGGCCACGGCAG	1561	1067	CUGCCGUGGCCUCUCCAGGAU	1808
1063	GGAGACGAGCUGGUGAAGC	1562	1063	GGAGACGAGCUGGUGAAGC	1562	1085	GCUUACACGAGCUCGUCUCC	1809
1081	CUGCCCCCGGAGCUGGCAG	1563	1081	CUGCCCCCGGAGCUGGCAG	1563	1103	CUGCCAGCUUACACGGGCAG	1810
1099	GCGUACCCCCCGCCCGAGU	1564	1099	GCGUACCCCCCGCCCGAGU	1564	1121	ACUCGGCGGGGGGUACGC	1811
1117	UUCGAGUGGUACAAGGAUG	1565	1117	UUCGAGUGGUACAAGGAUG	1565	1139	CAUCCUUGUACCACUGGAA	1812
1135	GGAAGGCACUGUCCGGGC	1566	1135	GGAAGGCACUGUCCGGGC	1566	1157	GCCCGACAGUGCCUUUCC	1813
1153	CGCCACAGUCCACAUGCC	1567	1153	CGCCACAGUCCACAUGCC	1567	1175	GGCAUGUGGACUGUGGCG	1814
1171	CUGGUGCUCAAGGAGUGA	1568	1171	CUGGUGCUCAAGGAGUGA	1568	1193	UCACCUCCUUGAGCACCCAG	1815
1189	ACAGAGGCCAGCACAGGCA	1569	1189	ACAGAGGCCAGCACAGGCA	1569	1211	UGCCUGUGCUGGCCUCUGU	1816
1207	ACCUACACCCUCGCCUCUGU	1570	1207	ACCUACACCCUCGCCUCUGU	1570	1229	ACAGGGCGAGGGGUGUAGGU	1817
1225	UGGAACUCCGUCGUGGCC	1571	1225	UGGAACUCCGUCGUGGCC	1571	1247	GGCCAGCAGCGGAGUCCA	1818
1243	CUGAGGCGCAACAUCAGCC	1572	1243	CUGAGGCGCAACAUCAGCC	1572	1265	GGCUGAUGUUGCGCCUCAG	1819
1261	CUGGAGCUGGUGGUGAAUG	1573	1261	CUGGAGCUGGUGGUGAAUG	1573	1283	CAUUCACACCACGCUCCAG	1820
1279	GUGCCCCCCCAGAUACAUG	1574	1279	GUGCCCCCCCAGAUACAUG	1574	1301	CAUGUAUCUGGGGGGCAC	1821
1297	GAGAAGGAGGCCUCCUCCC	1575	1297	GAGAAGGAGGCCUCCUCCC	1575	1319	GGGAGGAGGCCUCCUUCUC	1822
1315	CCCAGCAUCUACUCGCGUC	1576	1315	CCCAGCAUCUACUCGCGUC	1576	1337	GACGCGAGUAGUAGCUGGG	1823
1333	CACAGCCGCCAGGCCCUCA	1577	1333	CACAGCCGCCAGGCCCUCA	1577	1355	UGAGGGCCUGCGGCUGUG	1824
1351	ACCUGCACGGCCUACGGGG	1578	1351	ACCUGCACGGCCUACGGGG	1578	1373	CCCCGUAGGCCGUGCAGGU	1825
1369	GUGCCCCUGCCUUCACAGA	1579	1369	GUGCCCCUGCCUUCACAGA	1579	1391	UGCUGAGAGGCAGGGGCAC	1826
1387	AUCCAGUGGCACUGGCGGC	1580	1387	AUCCAGUGGCACUGGCGGC	1580	1409	GCCGCCAGUGCCACUGGAU	1827
1405	CCUUGGACACCCUGCAAGA	1581	1405	CCUUGGACACCCUGCAAGA	1581	1427	UCUUGCAGGGUGUCCAGGG	1828
1423	AUGUUUGCCCCAGCGUAGUC	1582	1423	AUGUUUGCCCCAGCGUAGUC	1582	1445	GACUACGCUGGGCAAAACAU	1829
1441	CUCGGCGGGCGGACGAGC	1583	1441	CUCGGCGGGCGGACGAGC	1583	1463	GCUGCUGCCCGCCCGGAG	1830
1459	CAAGACCUCAUGCCACAGU	1584	1459	CAAGACCUCAUGCCACAGU	1584	1481	ACUGUGGCAUGAGGUCUUG	1831
1477	UGCCGUGACUGGAGGGCGG	1585	1477	UGCCGUGACUGGAGGGCGG	1585	1499	CCGCCUCCAGUCACGGCA	1832
1495	GUGACCACGAGGAUGCCG	1586	1495	GUGACCACGAGGAUGCCG	1586	1517	CGGAUCCUCCGUGGUCAC	1833
1513	GUGAACCCCAUCGAGAGCC	1587	1513	GUGAACCCCAUCGAGAGCC	1587	1535	GGCUCUCGAUGGGGUUCAC	1834
1531	CUGGACACCCUGGACCCGAGU	1588	1531	CUGGACACCCUGGACCCGAGU	1588	1553	ACUCGGUCCAGGUGUCCAG	1835
1549	UUUGUGGAGGGAAAGAAUA	1589	1549	UUUGUGGAGGGAAAGAAUA	1589	1571	UAUUCUUUCCCCUCCACAAA	1836

1567	AAGACUGUGAGCAAGCUGG	1590	1567	AAGACUGUGAGCAAGCUGG	1590	1589	1589	CCAGCUUGCUCACAGUCUU	1837
1585	GUGAUCCAGAAUGCCAACG	1591	1585	GUGAUCCAGAAUGCCAACG	1591	1607	1607	CGUUGGCAUUCUGGAUCAC	1838
1603	GUGUCUGCCAUGUACAAGU	1592	1603	GUGUCUGCCAUGUACAAGU	1592	1625	1625	ACUUGUACAUUGGCAGACAC	1839
1621	UGUGUGGUCUCCAACAAGG	1593	1621	UGUGUGGUCUCCAACAAGG	1593	1643	1643	CCUUGUUGGAGACCACACA	1840
1639	GUGGGCCAGGAUGAGCGGC	1594	1639	GUGGGCCAGGAUGAGCGGC	1594	1661	1661	GCCGCUCAUCCUGGCCCCAC	1841
1657	CUCAUCUACUUCUAUGUGA	1595	1657	CUCAUCUACUUCUAUGUGA	1595	1679	1679	UCACAUAGAAGUAGAUGAG	1842
1675	ACCACCAUCCCGACGGCU	1596	1675	ACCACCAUCCCGACGGCU	1596	1697	1697	AGCCGUCGGGAUGGUGGU	1843
1693	UUCACCAUCGAAUCCAAGC	1597	1693	UUCACCAUCGAAUCCAAGC	1597	1715	1715	GCUUGGAUUCGAUGGUGAA	1844
1711	CCAUCCGAGGAGCUACUAG	1598	1711	CCAUCCGAGGAGCUACUAG	1598	1733	1733	CUAGUAGCUCCUCGGAUGG	1845
1729	GAGGGCCAGCCGGUGCUCC	1599	1729	GAGGGCCAGCCGGUGCUCC	1599	1751	1751	GGAGCACCGCGUGGCCCCUC	1846
1747	CUGAGCUGCCAAGCCGACA	1600	1747	CUGAGCUGCCAAGCCGACA	1600	1769	1769	UGUCGGCUUGGCAGCUCAG	1847
1765	AGCUACAAGUACGAGCAUC	1601	1765	AGCUACAAGUACGAGCAUC	1601	1787	1787	GAUGCUCGUACUUGUAGCU	1848
1783	CUGCGCUGGUACCGCCUCA	1602	1783	CUGCGCUGGUACCGCCUCA	1602	1805	1805	UGAGGCGGUACCGCGCAG	1849
1801	AACCUGUCCACGUCGACG	1603	1801	AACCUGUCCACGUCGACG	1603	1823	1823	CGUGCAGCGUGGACAGGUU	1850
1819	GAUGCGCACGGGAACCCGC	1604	1819	GAUGCGCACGGGAACCCGC	1604	1841	1841	GCGGGUUCGCGGCGCAUC	1851
1837	CUUCUGCUCGACUGCAAGA	1605	1837	CUUCUGCUCGACUGCAAGA	1605	1859	1859	UCUUGCAGUCGAGCAGAAG	1852
1855	AACGUGCAUCUGUUCGCCA	1606	1855	AACGUGCAUCUGUUCGCCA	1606	1877	1877	UGCGAACAGAUAGCACGUU	1853
1873	ACCCUCUGCCCGCCAGCC	1607	1873	ACCCUCUGCCCGCCAGCC	1607	1895	1895	GGCUGGCGGCCAGAGGGGU	1854
1891	CUGGAGGAGGUGGCACCUUG	1608	1891	CUGGAGGAGGUGGCACCUUG	1608	1913	1913	CAGGUGCCACCUCCUCCAG	1855
1909	GGGCGCGCCACGCCACGC	1609	1909	GGGCGCGCCACGCCACGC	1609	1931	1931	GCGUGGCGUGGCGCGCCCC	1856
1927	CUCAGCCUGAGUAUCCCCC	1610	1927	CUCAGCCUGAGUAUCCCCC	1610	1949	1949	GGGGAUACUCAGGCUGAG	1857
1945	CGGUCGCGCCCGAGCACG	1611	1945	CGGUCGCGCCCGAGCACG	1611	1967	1967	CGUGCUCGGGCGCGACGCG	1858
1963	GAGGGCCACUAUGUGUGCG	1612	1963	GAGGGCCACUAUGUGUGCG	1612	1985	1985	CGCACACAUAUGUGGCCUC	1859
1981	GAAGUGCAAGACCGCGCA	1613	1981	GAAGUGCAAGACCGCGCA	1613	2003	2003	UGCGCCGGUUCUUGCACUUC	1860
1999	AGCCAUGACAAGCACUGCC	1614	1999	AGCCAUGACAAGCACUGCC	1614	2021	2021	GGCAGUGCUUGUCAUGGCU	1861
2017	CACAAGAAGUACCUUGUCGG	1615	2017	CACAAGAAGUACCUUGUCGG	1615	2039	2039	CCGACAGGUACUUCUUGUG	1862
2035	GUGCAGGCCCCUGGAAGCCC	1616	2035	GUGCAGGCCCCUGGAAGCCC	1616	2057	2057	GGGCUUCCAGGGCCUCCAC	1863
2053	CCUCGGCUCACGCAGAACU	1617	2053	CCUCGGCUCACGCAGAACU	1617	2075	2075	AGUUCUGGUGAGCCGAGG	1864
2071	UUGACCGACCUCCUGGUGA	1618	2071	UUGACCGACCUCCUGGUGA	1618	2093	2093	UCACCAAGAGGUCGUGCAA	1865
2089	AACGUGAGCGACUCGCUUG	1619	2089	AACGUGAGCGACUCGCUUG	1619	2111	2111	CCAGCGAGUCGCUACGCUU	1866
2107	GAGAUGCAGUGCUUGGUGG	1620	2107	GAGAUGCAGUGCUUGGUGG	1620	2129	2129	CCACCAAGCACUGCAUCUC	1867
2125	GCCGGAGCGCACGCGCCCA	1621	2125	GCCGGAGCGCACGCGCCCA	1621	2147	2147	UGGGCGCGUGGCGCUCCGGC	1868
2143	AGCAUCGUGUGGUACAAG	1622	2143	AGCAUCGUGUGGUACAAG	1622	2165	2165	CUUUGUACCAACACGAUGCU	1869

2161	GACGAGAGGCGUCUGGAGG	1623	2161	GACGAGAGGCGUCUGGAGG	1623	2183	CCUCCAGCAGCCUCUCGUC	1870
2179	GAAGAUCUGGAGUCGACU	1624	2179	GAAGAUCUGGAGUCGACU	1624	2201	AGUCGACUCCAGACUUUUC	1871
2197	UUGCGGACUCCAACCAGA	1625	2197	UUGCGGACUCCAACCAGA	1625	2219	UCUGGUUGGAGUCCGCCAA	1872
2215	AAGCUGAGCAUCCAGCGCG	1626	2215	AAGCUGAGCAUCCAGCGCG	1626	2237	CGCGCUGGAUGCUCAGCUU	1873
2233	GUGCGGAGGAGGAUUGCGG	1627	2233	GUGCGGAGGAGGAUUGCGG	1627	2255	CCGCAUCCUCCUCGCGCAC	1874
2251	GGACCGUAUCUGUGCAGCG	1628	2251	GGACCGUAUCUGUGCAGCG	1628	2273	CGCUGCACAGAUACGGUCC	1875
2269	GUGUGCAGACCCAAAGGGCU	1629	2269	GUGUGCAGACCCAAAGGGCU	1629	2291	AGCCCUUGGGUCUCGACAC	1876
2287	UGCGUCAACUCCUCCGCCA	1630	2287	UGCGUCAACUCCUCCGCCA	1630	2309	UGGCGGAGGAGUUUGACGCA	1877
2305	AGCGUGGCCGUGGAAAGGCU	1631	2305	AGCGUGGCCGUGGAAAGGCU	1631	2327	AGCCUCCACGCGCCACGCU	1878
2323	UCCGAGGAUAAGGCAGCA	1632	2323	UCCGAGGAUAAGGCAGCA	1632	2345	UGCUGCCCUUAUCCUCGGA	1879
2341	AUGGAGAUUGUAUCCUUG	1633	2341	AUGGAGAUUGUAUCCUUG	1633	2363	CAAGGAUCACGAUCCCAU	1880
2359	GUCGGUACCGGCGUCAUCG	1634	2359	GUCGGUACCGGCGUCAUCG	1634	2381	CGAUGACGCCGGUACCGAC	1881
2377	GCUGUCUUUCUGGGUCC	1635	2377	GCUGUCUUUCUGGGUCC	1635	2399	GGACCCAGAAGAACAGCAGC	1882
2395	CUCCUCCUCCUCAUCUUCU	1636	2395	CUCCUCCUCCUCAUCUUCU	1636	2417	AGAAGAUGAGGAGGAGGAG	1883
2413	UGUAACAUGAGGAGGCCGG	1637	2413	UGUAACAUGAGGAGGCCGG	1637	2435	CCGGCCUCCUCAUGUUAACA	1884
2431	GCCACGCAGACAUAAGA	1638	2431	GCCACGCAGACAUAAGA	1638	2453	UCUUGAUGUCUGCGUGGGC	1885
2449	ACGGGCUACCGUCCAUCA	1639	2449	ACGGGCUACCGUCCAUCA	1639	2471	UGAUGGACAGGUAGCCCCU	1886
2467	AUCAUGGACCCCGGGAGG	1640	2467	AUCAUGGACCCCGGGAGG	1640	2489	CCUCCCCGGGUCUCAUGAU	1887
2485	GUGCCUCUGGAGGAGCAAU	1641	2485	GUGCCUCUGGAGGAGCAAU	1641	2507	AUUGCUCCUCCAGAGGCAC	1888
2503	UGCGAAUACCGUCCUACG	1642	2503	UGCGAAUACCGUCCUACG	1642	2525	CGUAGGACAGGUUUUCGCA	1889
2521	GAUGCCAGCCAGUGGGAAU	1643	2521	GAUGCCAGCCAGUGGGAAU	1643	2543	AUUCCACUGGCGUGGCAUC	1890
2539	UUCCCCCAGAGCGGCUGC	1644	2539	UUCCCCCAGAGCGGCUGC	1644	2561	GCAGCCGCUUCUCCCGGAA	1891
2557	CACCUUGGGAGAGUGCUCG	1645	2557	CACCUUGGGAGAGUGCUCG	1645	2579	CGAGCACUCUCCCGAGGUG	1892
2575	GGCUACGGCGCCUUCGGGA	1646	2575	GGCUACGGCGCCUUCGGGA	1646	2597	UCCCGAAGGCGCCCGUAGCC	1893
2593	AAGGUGGUGGAAGCCUCCG	1647	2593	AAGGUGGUGGAAGCCUCCG	1647	2615	CGGAGGCUUCCACCACCUU	1894
2611	GCUUUCGGCAUCCACAAGG	1648	2611	GCUUUCGGCAUCCACAAGG	1648	2633	CCUUGUGGAUGCCCGAAAGC	1895
2629	GGCAGCAGCUGUGACACCG	1649	2629	GGCAGCAGCUGUGACACCG	1649	2651	CGGUGUCACAGCUGCUGCC	1896
2647	GUGCCCGUGAAAUGCUGA	1650	2647	GUGCCCGUGAAAUGCUGA	1650	2669	UCAGCAUUUACACGGCCAC	1897
2665	AAAGAGGGGCCACCGCCA	1651	2665	AAAGAGGGGCCACCGCCA	1651	2687	UGGCCGUGGCGCCUUCUUU	1898
2683	AGCAGCAGCGCGCGCUGA	1652	2683	AGCAGCAGCGCGCGCUGA	1652	2705	UCAGCGCGCGCUGCUGCU	1899
2701	AUGUCGGAGCUCAAAGAUCC	1653	2701	AUGUCGGAGCUCAAAGAUCC	1653	2723	GGAUCUUAGAGCUCUCCGACAU	1900
2719	CUCAUUCACAUCGGCAACC	1654	2719	CUCAUUCACAUCGGCAACC	1654	2741	GGUUGCCGAUGUGAAUGAG	1901
2737	CACCUCAACGUGGUGCAACC	1655	2737	CACCUCAACGUGGUGCAACC	1655	2759	GGUUGACCACCGUUGAGGUG	1902

2755	CUCCUCGGGGCGUGCACCA	1656	2755	CUCCUCGGGGCGUGCACCA	1656	2777	UGGUGCACGCCCCCGAGGAG	1903
2773	AAGCCGAGGGCCCCCUCA	1657	2773	AAGCCGAGGGCCCCCUCA	1657	2795	UGAGGGGGCCUGCGGCUU	1904
2791	AUGGUGAUCGUGGAGUUCU	1658	2791	AUGGUGAUCGUGGAGUUCU	1658	2813	AGAACUCCACGAUACCAU	1905
2809	UGCAAGUACGGCAACCUUCU	1659	2809	UGCAAGUACGGCAACCUUCU	1659	2831	AGAGGUUGCCGUACUUGCA	1906
2827	UCCAACUUCUGCGCGCCA	1660	2827	UCCAACUUCUGCGCGCCA	1660	2849	UGGCGCGCAGGAAGUUGGA	1907
2845	AAGCGGAGCCCUUACAGCC	1661	2845	AAGCGGAGCCCUUACAGCC	1661	2867	GGCUGAAGGCGUCCCGCUU	1908
2863	CCUGCGCGGAGAAAGUCUC	1662	2863	CCUGCGCGGAGAAAGUCUC	1662	2885	GAGACUUCUCCGCGCAGGG	1909
2881	CCGAGCAGCGCGGACGCU	1663	2881	CCGAGCAGCGCGGACGCU	1663	2903	AGCGUCCGCGCUGCUCGGG	1910
2899	UUCGCGCCAUUGGUGGAGC	1664	2899	UUCGCGCCAUUGGUGGAGC	1664	2921	GCUCCACCAUGGCGCGGAA	1911
2917	CUCGCCAGGCUUGAUCGGA	1665	2917	CUCGCCAGGCUUGAUCGGA	1665	2939	UCCGAUCCAGCCUGGCGAG	1912
2935	AGGCGGCGGGGAGCAGCG	1666	2935	AGGCGGCGGGGAGCAGCG	1666	2957	CGCUGUCCCGCGCGCCU	1913
2953	GACAGGCUCCUUCGCGC	1667	2953	GACAGGCUCCUUCGCGC	1667	2975	GC GCGAAGAGGACCCUGUC	1914
2971	CGGUUCUCGAAGACCGAGG	1668	2971	CGGUUCUCGAAGACCGAGG	1668	2993	CCUCGGUUCUUCGAGAACC	1915
2989	GGCGGAGCGAGCGGGCUU	1669	2989	GGCGGAGCGAGCGGGCUU	1669	3011	AAGCCCGCCUCGCUCCGCC	1916
3007	UCUCCAGACCAAGAAAGCUG	1670	3007	UCUCCAGACCAAGAAAGCUG	1670	3029	CAGCUUCUUGGUCUGGAGA	1917
3025	GAGGACCUUGGCGUGAGCC	1671	3025	GAGGACCUUGGCGUGAGCC	1671	3047	GGCUCAGCCACAGGUCCUC	1918
3043	CCGUGACCAUGGAAGAUC	1672	3043	CCGUGACCAUGGAAGAUC	1672	3065	GAUCUCCAUGGUCAGCGG	1919
3061	CUUGUCUGCUACAGCUUCC	1673	3061	CUUGUCUGCUACAGCUUCC	1673	3083	GGAAGCUGUAGCAGACAAG	1920
3079	CAGGUGGCCAGAGGGAUGG	1674	3079	CAGGUGGCCAGAGGGAUGG	1674	3101	CCAUCUCCUGGCCACCUG	1921
3097	GAGUUCUUGGCUUCCCGAA	1675	3097	GAGUUCUUGGCUUCCCGAA	1675	3119	UUCGGGAAGCCAGGAACUC	1922
3115	AAGUGCAUCCACAGAGACC	1676	3115	AAGUGCAUCCACAGAGACC	1676	3137	GGUCUCUGUGGAUGCACUU	1923
3133	CUGGCUUCUCGGAACAUC	1677	3133	CUGGCUUCUCGGAACAUC	1677	3155	GAAUGUCCGAGCAGCCAG	1924
3151	CUGCUGUCGGAAGCGACG	1678	3151	CUGCUGUCGGAAGCGACG	1678	3173	CGUCGCUUCCGACAGCAG	1925
3169	GUGGUGAAGAUUCUGUGACU	1679	3169	GUGGUGAAGAUUCUGUGACU	1679	3191	AGUCACAGAUUCUACCCAC	1926
3187	UUUGCCUUGCCCGGACA	1680	3187	UUUGCCUUGCCCGGACA	1680	3209	UGUCCCGGGCAAGGCCAAA	1927
3205	AUCUACAAAGACCCCGACU	1681	3205	AUCUACAAAGACCCCGACU	1681	3227	AGUCGGGUCUUIUGUAGAU	1928
3223	UACGUCGCAAGGGCAGUG	1682	3223	UACGUCGCAAGGGCAGUG	1682	3245	CACUGCCUUGCGGACGUA	1929
3241	GCCCGGCGCCCCUGAAGU	1683	3241	GCCCGGCGCCCCUGAAGU	1683	3263	ACUUCAGGGCAGCCGGGC	1930
3259	UGGAUGGCCCCUGAAAGCA	1684	3259	UGGAUGGCCCCUGAAAGCA	1684	3281	UGCUIUCAGGGGCCAUCCA	1931
3277	AUCUUCGACAAGGUGUACA	1685	3277	AUCUUCGACAAGGUGUACA	1685	3299	UGUACACCUUGUCGAAGAU	1932
3295	ACCACGCAGAGUACGUGU	1686	3295	ACCACGCAGAGUACGUGU	1686	3317	ACACGUCACUCUGCGUGU	1933
3313	UGGUCCUUGGGGUGCUUC	1687	3313	UGGUCCUUGGGGUGCUUC	1687	3335	GAAGCACCCCAAAGGACCA	1934
3331	CUCUGGGAGAUUCUUCUC	1688	3331	CUCUGGGAGAUUCUUCUC	1688	3353	GAGAGAAAGAUUCUCCAGAG	1935

3349	CUGGGGGCCUCCCCGUACC	1689	3349	CUGGGGGCCUCCCCGUACC	1689	3371	GGUACGGGGAGGCCCCCAG	1936
3367	CCUGGGGUGCAGAUCAAUG	1690	3367	CCUGGGGUGCAGAUCAAUG	1690	3389	CAUUGAUCUGCACCACCAGG	1937
3385	GAGGAGUUCUGCCAGCGCG	1691	3385	GAGGAGUUCUGCCAGCGCG	1691	3407	CGCGCUGGCAGAAACUCCUC	1938
3403	GUGAGAGACGGCACAAAGGA	1692	3403	GUGAGAGACGGCACAAAGGA	1692	3425	UCCUUGUGCCGUCUCUCAC	1939
3421	AUGAGGGCCCCGGAGCUGG	1693	3421	AUGAGGGCCCCGGAGCUGG	1693	3443	CCAGCUCGGGGCCCCUCAU	1940
3439	GCCACUCCCGCCCAUACGCC	1694	3439	GCCACUCCCGCCCAUACGCC	1694	3461	GGCGUAUGGGGGGAGUGGC	1941
3457	CACAUCAUGCUGAAACUCGU	1695	3457	CACAUCAUGCUGAAACUCGU	1695	3479	AGCAGUUCAGCAUGAUGUG	1942
3475	UGGUCCGGAGACCCCAAGG	1696	3475	UGGUCCGGAGACCCCAAGG	1696	3497	CCUUGGGGUCUCCGGACCA	1943
3493	GCGAGACCUGCAUUCUCGG	1697	3493	GCGAGACCUGCAUUCUCGG	1697	3515	CCGAGAAUGCAGGUCUCGC	1944
3511	GACCUGGUGGAGAUCCUGG	1698	3511	GACCUGGUGGAGAUCCUGG	1698	3533	CCAGGAUCUCCACCAGGUC	1945
3529	GGGACCUUGCUCCAGGGCA	1699	3529	GGGACCUUGCUCCAGGGCA	1699	3551	UGCCCUGGAGCAGGUCCCC	1946
3547	AGGGGCCUGCAAAGAGGAAG	1700	3547	AGGGGCCUGCAAAGAGGAAG	1700	3569	CUUCCUCUUGCAGGCCCCU	1947
3565	GAGGAGGUCUGAUGGCC	1701	3565	GAGGAGGUCUGAUGGCC	1701	3587	GGGCCAUGCAGACCUCUCUC	1948
3583	CCGCGCAGCUCUCAGAGCU	1702	3583	CCGCGCAGCUCUCAGAGCU	1702	3605	AGCUCUGAGAGCUCGCGGG	1949
3601	UCAGAAAGAGGCGAGCUUCU	1703	3601	UCAGAAAGAGGCGAGCUUCU	1703	3623	AGAAAGCUGCCCUUCUGA	1950
3619	UCGCAGGUGUCCACCAUGG	1704	3619	UCGCAGGUGUCCACCAUGG	1704	3641	CCAUGGUGGACACCUCGGA	1951
3637	GCCCUACACAUCCGCCCAGG	1705	3637	GCCCUACACAUCCGCCCAGG	1705	3659	CCUGGGCGAUGUGUAGGGC	1952
3655	GCUGACGUGAGGACAGCC	1706	3655	GCUGACGUGAGGACAGCC	1706	3677	GGCUGUCCUCAGCGUCAGC	1953
3673	CCGCCAAGCCUGCAGCGCC	1707	3673	CCGCCAAGCCUGCAGCGCC	1707	3695	GGCGCUGCAGGCUUGGCGG	1954
3691	CACAGCCUGCCCGCCAGGU	1708	3691	CACAGCCUGCCCGCCAGGU	1708	3713	ACCUGGGGCCAGGCUGUG	1955
3709	UAUUACAACUGGGUGUCCU	1709	3709	UAUUACAACUGGGUGUCCU	1709	3731	AGGACACCCAGUUGUAAUA	1956
3727	UUUCCCGGUGCCUGGCCA	1710	3727	UUUCCCGGUGCCUGGCCA	1710	3749	UGGCCAGGCACCCGGGAAA	1957
3745	AGAGGGCUGAGACCCGUG	1711	3745	AGAGGGCUGAGACCCGUG	1711	3767	CACGGGUCUCAGCCCCUCU	1958
3763	GGUCCUCCAGGAUGAAGA	1712	3763	GGUCCUCCAGGAUGAAGA	1712	3785	UCUUCAUCCUGGAGGAACC	1959
3781	ACAUUUGAGGAUUUCCCCA	1713	3781	ACAUUUGAGGAUUUCCCCA	1713	3803	UGGGAAUUCUCAAUUGU	1960
3799	AUGACCCCAACGACCUACA	1714	3799	AUGACCCCAACGACCUACA	1714	3821	UGUAGGUCUUGGGGUCAU	1961
3817	AAAGGCUCUGGACAACC	1715	3817	AAAGGCUCUGGACAACC	1715	3839	GGUUGUCCACAGAGCCUUU	1962
3835	CAGACAGACAGUGGGAUGG	1716	3835	CAGACAGACAGUGGGAUGG	1716	3857	CCAUCCACUGUCUGUCUG	1963
3853	GUGCUGGCCUCCGGAGGAGU	1717	3853	GUGCUGGCCUCCGGAGGAGU	1717	3875	ACUCCUCCAGGCCAGCAC	1964
3871	UUUGAGCAGAUAGAGGCA	1718	3871	UUUGAGCAGAUAGAGGCA	1718	3893	UGCUCUCUAUCUGCUCAAA	1965
3889	AGGCAUAGACAAGAAAGCG	1719	3889	AGGCAUAGACAAGAAAGCG	1719	3911	CGCUUCUUCUGUCUAUGCCU	1966
3907	GGCUUCAGGUAGCUGAAGC	1720	3907	GGCUUCAGGUAGCUGAAGC	1720	3929	GCUUCAGCUACCUGAAGCC	1967
3925	CAGAGAGAGAGAAGGCAGC	1721	3925	CAGAGAGAGAGAAGGCAGC	1721	3947	GCUGCCUUCUCUCUCUCUG	1968

3943	CAUACGUCAGCAUUUUCUU	1722	3943	CAUACGUCAGCAUUUUCUU	1722	3965	AAGAAAAUGCUGACGUAUG	1969
3961	UCUCUGCACUUUAAGAAA	1723	3961	UCUCUGCACUUUAAGAAA	1723	3983	UUUCUUUAAGUGCAGAGA	1970
3979	AGAUAAGACUUUAAGAC	1724	3979	AGAUAAGACUUUAAGAC	1724	4001	GUCUAAAGUCUUUGAUCU	1971
3997	CUUUCGUAUUUCUUCUAC	1725	3997	CUUUCGUAUUUCUUCUAC	1725	4019	GUAGAGAAUUAAGCGAAAG	1972
4015	CUGCUAUCUACUACAAACU	1726	4015	CUGCUAUCUACUACAAACU	1726	4037	AGUUUGUAGUAGAUAGCAG	1973
4033	UUCAAAAGAGGAACCCAGGAG	1727	4033	UUCAAAAGAGGAACCCAGGAG	1727	4055	CUCUUGGUUCCUCUUUGAA	1974
4051	GGACAAGAGGAGCAUGAAA	1728	4051	GGACAAGAGGAGCAUGAAA	1728	4073	UUUCAUGCUCUCCUUGUCC	1975
4069	AGUGGACAAGGAGUGUGAC	1729	4069	AGUGGACAAGGAGUGUGAC	1729	4091	GUCACACUCCUUGUCCACU	1976
4087	CCACUGAAGCACACACAGGG	1730	4087	CCACUGAAGCACACACAGGG	1730	4109	CCCUGUGGUGCUUCAGUGG	1977
4105	GAGGGUUAAGGCCUCCGGA	1731	4105	GAGGGUUAAGGCCUCCGGA	1731	4127	UCCGGAGGCCUAAACCCUC	1978
4123	AUGACUGCGGCAGGCCUUG	1732	4123	AUGACUGCGGCAGGCCUUG	1732	4145	CAGGCCUGCCCCGAGUCAU	1979
4141	GGAUAAUUAUCCAGCCUCCC	1733	4141	GGAUAAUUAUCCAGCCUCCC	1733	4163	GGGAGGUGGAUUAUUAUCC	1980
4159	CACAAGAGCUGGUGGAGC	1734	4159	CACAAGAGCUGGUGGAGC	1734	4181	GCUCCACCAGCUUCUUGUG	1981
4177	CAGAGUUAUCCUGACUCC	1735	4177	CAGAGUUAUCCUGACUCC	1735	4199	GGAGUCAGGGAACACUCUG	1982
4195	CUCCAAGGAAAGGAGACG	1736	4195	CUCCAAGGAAAGGAGACG	1736	4217	CGUCUCCCUUCCUUGGAG	1983
4213	GCCUUUAUUGGUCUGCUG	1737	4213	GCCUUUAUUGGUCUGCUG	1737	4235	CAGCAGACCAUGAAAGGGC	1984
4231	GAGUAACAGGUGCCUUC	1738	4231	GAGUAACAGGUGCCUUC	1738	4253	GGGAAGGCCUUGUACUC	1985
4249	CAGACACUGGCGUUAUCUG	1739	4249	CAGACACUGGCGUUAUCUG	1739	4271	GCAGUAACGCCAGUGUCUG	1986
4267	CUUGACCAAGAGCCCUCA	1740	4267	CUUGACCAAGAGCCCUCA	1740	4289	UGAGGGCUCUUGGUCUAA	1987
4285	AAGCGCCCUUAUGCCAGC	1741	4285	AAGCGCCCUUAUGCCAGC	1741	4307	GCUGGCAUAAGGCCCGCUU	1988
4303	CGUGACAGAGGCUACACCU	1742	4303	CGUGACAGAGGCUACACCU	1742	4325	AGGUGAGCCUUCUGACAG	1989
4321	UCUUGCCUUAUAGGUCACU	1743	4321	UCUUGCCUUAUAGGUCACU	1743	4343	AGUGACCUAGAAGGCAAGA	1990
4339	UUCUCACAAUGUCCCUUCA	1744	4339	UUCUCACAAUGUCCCUUCA	1744	4361	UGAAGGGACAUUGUGAGAA	1991
4357	AGCACCUAGCCUUGGCC	1745	4357	AGCACCUAGCCUUGGCC	1745	4379	GGGCACAGGGUCAGGUGCU	1992
4375	CGCCGAUUAUCCUUGGUA	1746	4375	CGCCGAUUAUCCUUGGUA	1746	4397	UACCAAGGAUUAUUCGGCG	1993
4393	AAUAUGAGUAAUACAUCAA	1747	4393	AAUAUGAGUAAUACAUCAA	1747	4415	UUGAUGUAUUAUCUCAUUA	1994
4411	AAGAGUAGUAAUAAAAGCU	1748	4411	AAGAGUAGUAAUAAAAGCU	1748	4433	AGCUUUUAUUAUUAUUAUUA	1995
4429	UAAUUAUUAUUAUUAUUA	1749	4429	UAAUUAUUAUUAUUAUUA	1749	4451	UUAUAAACAUGAUUAUUAUUA	1996

The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhanging sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhanging sequence of the lower sequence is optionally complementary to a portion of the target sequence. The overhang can comprise the general

structure NN or NsN, where N stands for any nucleotide (e.g., thymidine) and s stands for phosphorothioate or other internucleotide linkage as described herein (e.g. internucleotide linkage having Formula I). The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII or any combination thereof (see for example chemical modifications as shown in Table V herein).

Table III: VEGFr Synthetic Modified siNA constructs

VEGFR1

Target	Seq ID	COMPOUND#	Aliases	Sequence	Seq ID
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:298U21 siRNA sense	UGUCUGCUUCUCACAGGAUTT	2020
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1956U21 siRNA sense	AGGAGAGGACCUGAAACUGTT	2021
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1957U21 siRNA sense	GGAGAGGACCUGAAACUGUTT	2022
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2787U21 siRNA sense	AUUUGGCAUUUAGAAAUACATT	2023
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:316L21 siRNA (298C) antisense	AUCCUGUGAGAAAGCAGACATT	2024
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1974L21 siRNA (1956C) antisense	CAGUUUCAGGUCCUCUCUCCUTT	2025
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1975L21 siRNA (1957C) antisense	ACAGUUUCAGGUCCUCUCUCCITT	2026
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2805L21 siRNA (2787C) antisense	UGAUUUUCUUAAUGCCAAAUTT	2027
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:298U21 siRNA stab04 sense	B uGucuGcuucucAcAGGAuTT B	2028
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1956U21 siRNA stab04 sense	B AGGAGAGGACcuGAAAcuGTT B	2029
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1957U21 siRNA stab04 sense	B GGAGAGGACcuGAAAcuGUTT B	2030
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2787U21 siRNA stab04 sense	B AuuuGGcAuuuAAGAAAUacATT B	2031
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:316L21 siRNA (298C) stab05 antisense	AuccuGuGAGAA GcAGAcATsT	2032
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1974L21 siRNA (1956C) stab05 antisense	cAGuuucAGGuccucuccuTsT	2033
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1975L21 siRNA (1957C) stab05 antisense	AcAGuuucAGGuccucuccTsT	2034
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2805L21 siRNA (2787C) stab05 antisense	uGAuuucuuAAuGccAAAUtsT	2035
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:298U21 siRNA stab07 sense	B uGucuGcuucucAcAGGAuTT B	2036
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1956U21 siRNA stab07 sense	B AGGAGAGGACcuGAAAcuGTT B	2037
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1957U21 siRNA stab07 sense	B GGAGAGGACcuGAAAcuGUTT B	2038
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2787U21 siRNA stab07 sense	B AuuuGGcAuuuAAGAAAUacATT B	2039
GCUGUCGCUUCUCACAGGAUCU	1997		FLT1:316L21 siRNA (298C) stab11 antisense	AuccuGuGAGAA GcAGAcATsT	2040
GAAGGAGAGGACCUGAAACUGUC	1998		FLT1:1974L21 siRNA (1956C) stab11 antisense	cAGuuucAGGuccucuccuTsT	2041
AAGGAGAGGACCUGAAACUGUCU	1999		FLT1:1975L21 siRNA (1957C) stab11 antisense	AcAGuuucAGGuccucuccTsT	2042
GCAUUUGGCAUUUAGAAAUACACC	2000		FLT1:2805L21 siRNA (2787C) stab11 antisense	uGAuuucuuAAuGccAAAUtsT	2043
AACUGAGUUUUAAAAGGCACCCAG	2009	31209	FLT1:367L21 siRNA (349C) stab05 inv antisense	GAcucAAAAuuuuuccGuGGGTsT	2176
AAGCAAGGAGGGCCUCUGAUGGU	2012	31210	FLT1:2967L21 siRNA (2949C) stab05 inv antisense	cGuuccucccccGGAGAcuAcTsT	2177

AGCCUGGAAAGAAUCAAACCCUU	2011	31211	FLT1:3930L21 siRNA (3912C) stab05 inv antisense	GGAccuuuuuuAGuuuuGGTsT	2178
AACUGAGUUUUAAAAGGCACCCAG	2009	31212	FLT1:349U21 siRNA stab07 inv sense	B cccAcGGAAAAuuuuGAGucTT B	2179
AAGCAAGGAGGGCCUCUGAUGGU	2012	31213	FLT1:2949U21 siRNA stab07 inv sense	B GuAGucuccGGGAGGAACGTT B	2180
AGCCUGGAAAGAAUCAAACCCUU	2011	31214	FLT1:3912U21 siRNA stab07 inv sense	B ccAAAAcuAAGAAAGGuccTT B	2181
AACUGAGUUUUAAAAGGCACCCAG	2009	31215	FLT1:367L21 siRNA (349C) stab08 inv antisense	GAcuAAAAuuuuuccGuGGGTsT	2182
AAGCAAGGAGGGCCUCUGAUGGU	2012	31216	FLT1:2967L21 siRNA (2949C) stab08 inv antisense	cGuuuccuccGGAGAGuAcTsT	2183
AGCCUGGAAAGAAUCAAACCCUU	2011	31217	FLT1:3930L21 siRNA (3912C) stab08 inv antisense	GGAccuuuuuuAGuuuuGGTsT	2184
AACUGAGUUUUAAAAGGCACCCAG	2009	31270	FLT1:349U21 siRNA stab09 sense	B CUGAGUUUUAAAAGGCACCCCTT B	2185
AAGCAAGGAGGGCCUCUGAUGGU	2012	31271	FLT1:2949U21 siRNA stab09 sense	B GCAAGGAGGGCCUCUGAUGTT B	2186
AGCCUGGAAAGAAUCAAACCCUU	2011	31272	FLT1:3912U21 siRNA stab09 sense	B CCUGGAAAGAAUCAAACCCCTT B	2187
AACUGAGUUUUAAAAGGCACCCAG	2009	31273	FLT1:367L21 siRNA (349C) stab10 antisense	GGGUGCCUUUUAAAACUCAGTsT	2188
AAGCAAGGAGGGCCUCUGAUGGU	2012	31274	FLT1:2967L21 siRNA (2949C) stab10 antisense	CAUCAGAGGCCCCUCCUUGCTsT	2189
AGCCUGGAAAGAAUCAAACCCUU	2011	31275	FLT1:3930L21 siRNA (3912C) stab10 antisense	GGUUUUUAUUUUUCCAGGTsT	2190
AACUGAGUUUUAAAAGGCACCCAG	2009	31276	FLT1:349U21 siRNA stab09 inv sense	B CCCACGGAAAAUUUGAGUCTT B	2191
AAGCAAGGAGGGCCUCUGAUGGU	2012	31277	FLT1:2949U21 siRNA stab09 inv sense	B GUAGUCUCCGGGAGGAACGTT B	2192
AGCCUGGAAAGAAUCAAACCCUU	2011	31278	FLT1:3912U21 siRNA stab09 inv sense	B CCAAAACUAAAGAAAGGUCCCTT B	2193
AACUGAGUUUUAAAAGGCACCCAG	2009	31279	FLT1:367L21 siRNA (349C) stab10 inv antisense	GACUCAAUUUUUCCGUGGGTsT	2194
AAGCAAGGAGGGCCUCUGAUGGU	2012	31280	FLT1:2967L21 siRNA (2949C) stab10 inv antisense	CGUUCCUCCCGGAGACUACTsT	2195
AGCCUGGAAAGAAUCAAACCCUU	2011	31281	FLT1:3930L21 siRNA (3912C) stab10 inv antisense	GGACCUUUUCUUAUUUUUGGTsT	2196
AACAACCCACAAAAUACAACAAGA	2010	31424	FLT1:2358L21 siRNA (2340C) stab11 3'-BrdU antisense	uuGuuGuAuuuuuGuGGuuGXsX	2197
AAGCAAGGAGGGCCUCUGAUGGU	2012	31425	FLT1:2967L21 siRNA (2949C) stab11 3'-BrdU antisense	cAucAGAGGccuccuuGcXsX	2198
AACAACCCACAAAAUACAACAAGA	2010	31442	FLT1:2358L21 siRNA (2340C) stab11 3'-BrdU antisense	uuGuuGuAuuuuuGuGGuuGXsT	2199
AAGCAAGGAGGGCCUCUGAUGGU	2012	31443	FLT1:2967L21 siRNA (2949C) stab11 3'-BrdU antisense	cAucAGAGGccuccuuGcXsT	2200
AACAACCCACAAAAUACAACAAGA	2010	31449	FLT1:2340U21 siRNA stab09 sense	B CAACCCACAAAAUACAACAATT B	2201
AACAACCCACAAAAUACAACAAGA	2010	31450	FLT1:2340U21 siRNA inv stab09 sense	B AACAAACAUAAAACACCAACTT B	2202
AACAACCCACAAAAUACAACAAGA	2010	31451	FLT1:2358L21 siRNA (2340C) stab10 antisense	UUGUUGUAUUUUUGUGGUUGTsT	2203
AACAACCCACAAAAUACAACAAGA	2010	31452	FLT1:2358L21 siRNA (2340C) inv stab10 antisense	GUUGGUGUUUAUUGUUUGUUTsT	2204

AACAACCCACAAAAUACAACAAGA	2010	31509	FLT1:2358L21 siRNA (2340C) stab11 antisense	uuGuuGuuuuuGuGGuuGTsT	2217
AACUGAGUUUUAAAAGGCACCCAG	2009	31794	2x cholesterol + R31194 FLT1:349U21 siRNA stab07 sense	(H)2 ZTa B cuGAGuuuuAAAAAGGcAcccTT B	2218
AACUGAGUUUUAAAAGGCACCCAG	2009	31795	2x cholesterol + R31212 FLT1:349U21 siRNA stab07 inv sense	(H)2 ZTa B cccAcGGAAAAuuuGAGucTT B	2219
AACUGAGUUUUAAAAGGCACCCAG	2009	31796	2x cholesterol + R31270 FLT1:349U21 siRNA stab09 sense	(H)2 ZTa B	2220
AACUGAGUUUUAAAAGGCACCCAG	2009	31797	2x cholesterol + R31276 FLT1:349U21 siRNA stab09 inv sense	(H)2 ZTa B	2221
AACUGAGUUUUAAAAGGCACCCAG	2009	31798	2x C18 phospholipid + R31194 FLT1:349U21 siRNA stab07 sense	CCCACGGAAAAUUUGAGUcTT B	2222
AACUGAGUUUUAAAAGGCACCCAG	2009	31799	2x C18 phospholipid + R31212 FLT1:349U21 siRNA stab07 inv sense	(L)2 ZTa B cuGAGuuuuAAAAAGGcAcccTT B	2223
AACUGAGUUUUAAAAGGCACCCAG	2009	31800	2x C18 phospholipid + R31270 FLT1:349U21 siRNA stab09 sense	(L)2 ZTa B	2224
AACUGAGUUUUAAAAGGCACCCAG	2009	31801	2x C18 phospholipid + R31276 FLT1:349U21 siRNA stab09 inv sense	(L)2 ZTa B	2225
CAUGCUGGACUGCUGGCAC	2244	32235	FLT1:3645U21 siRNA sense	CAUGCUGGACUGCUGGCACcTT	2275
AUGCUGGACUGCUGGCACA	2245	32236	FLT1:3646U21 siRNA sense	AUGCUGGACUGCUGGCACATT	2276
UGCUGGACUGCUGGCACAG	2246	32237	FLT1:3647U21 siRNA sense	UGCUGGACUGCUGGCACAGTT	2277
CAUGCUGGACUGCUGGCAC	2244	32250	FLT1:3663L21 siRNA (3645C) antisense	GUGCCAGCAGUCCAGCAUGTT	2278
AUGCUGGACUGCUGGCACA	2245	32251	FLT1:3664L21 siRNA (3646C) antisense	UGUGCCAGCAGUCCAGCAUTT	2279
UGCUGGACUGCUGGCACAG	2246	32252	FLT1:3665L21 siRNA (3647C) antisense	CUGUGCCAGCAGUCCAGCATT	2280
AACUGAGUUUUAAAAGGCACCCAG	2009	32278	FLT1:349U21 siRNA stab16 sense	B CUgagUUUaaaggCaCCcTT B	2281
AACUGAGUUUUAAAAGGCACCCAG	2009	32279	FLT1:349U21 siRNA stab18 sense	B cuGAGuuuuAAAAAGGcAcccTT B	2282
AACUGAGUUUUAAAAGGCACCCAG	2009	32280	FLT1:349U21 siRNA inv stab16 sense	B CCcAGgaaaaUUUgagUcTT B	2283
AACUGAGUUUUAAAAGGCACCCAG	2009	32281	FLT1:349U21 siRNA inv stab18 sense	B cccAcGGAAAAuuuGAGucTT B	2284
CUGAACUGAGUUUUAAAAGGCACCC	2247	32282	FLT1:346U21 siRNA stab09 sense	B GAACUGAGUUUUAAAAGGCATT B	2285
UGAACUGAGUUUUAAAAGGCACCC	2248	32283	FLT1:347U21 siRNA stab09 sense	B AACUGAGUUUUAAAAGGCATT B	2286
GAACUGAGUUUUAAAAGGCACCCCA	2249	32284	FLT1:348U21 siRNA stab09 sense	B ACUGAGUUUUAAAAGGCACcTT B	2287
ACUGAGUUUUAAAAGGCACCCAGC	2250	32285	FLT1:350U21 siRNA stab09 sense	B UGAGUUUUAAAAGGCACCCATT B	2288
CUGAGUUUUAAAAGGCACCCAGCA	2251	32286	FLT1:351U21 siRNA stab09 sense	B GAGUUUUAAAAGGCACCCAGTT B	2289
UGAGUUUUAAAAGGCACCCAGCAC	2252	32287	FLT1:352U21 siRNA stab09 sense	B AGUUUUAAAAGGCACCCAGcTT B	2290
GAGUUUUAAAAGGCACCCAGCACA	2253	32288	FLT1:353U21 siRNA stab09 sense	B GUUUUUAAAAGGCACCCAGCATT B	2291
CUGAACUGAGUUUUAAAAGGCACCC	2247	32289	FLT1:364L21 siRNA (346C) stab10 antisense	UGCCUUUUAAAACUCAGUUcTsT	2292
UGAACUGAGUUUUAAAAGGCACCC	2248	32290	FLT1:365L21 siRNA (347C) stab10 antisense	GUGCCUUUUAAAACUCAGUUcTsT	2293
GAACUGAGUUUUAAAAGGCACCCCA	2249	32291	FLT1:366L21 siRNA (348C) stab10 antisense	GGUGCCUUUUAAAACUCAGUcTsT	2294
ACUGAGUUUUAAAAGGCACCCAGC	2250	32292	FLT1:368L21 siRNA (350C) stab10 antisense	UGGGUGCCUUUUAAAACUCATsT	2295

				antisense		
CUGAGUUUAAAAGGCACCCAGCA	2251	32293	antisense	FLT1:369L21 siRNA (351C) stab10		CUUGGUGCCUUUUAAACUCTsT
UGAGUUUAAAAGGCACCCAGCAC	2252	32294	antisense	FLT1:370L21 siRNA (352C) stab10		GCUGGUGCCUUUUAAACUTsT
GAGUUUAAAAGGCACCCAGCACA	2253	32295	antisense	FLT1:371L21 siRNA (353C) stab10		UGCUGGGUGCCUUUUAAAACtTsT
CUGAACUGAGUUUAAAAGGCACC	2247	32296	antisense	FLT1:346U21 siRNA inv stab09 sense		B ACGGAAAAUUUGAGUCAAGTT B
UGAACUGAGUUUAAAAGGCACCC	2248	32297	antisense	FLT1:347U21 siRNA inv stab09 sense		B CACGGAAAAUUUGAGUCAATT B
GAACUGAGUUUAAAAGGCACCCA	2249	32298	antisense	FLT1:348U21 siRNA inv stab09 sense		B CCACGGAAAAUUUGAGUCATT B
ACUGAGUUUAAAAGGCACCCAGC	2250	32299	antisense	FLT1:350U21 siRNA inv stab09 sense		B ACCCACGGAAAAUUUGAGUTT B
CUGAGUUUAAAAGGCACCCAGCA	2251	32300	antisense	FLT1:351U21 siRNA inv stab09 sense		B GACCCACGGAAAAUUUGAGTT B
UGAGUUUAAAAGGCACCCAGCAC	2252	32301	antisense	FLT1:352U21 siRNA inv stab09 sense		B CGACCCACGGAAAAUUUGATT B
GAGUUUAAAAGGCACCCAGCACA	2253	32302	antisense	FLT1:353U21 siRNA inv stab09 sense		B ACGACCCACGGAAAAUUUGTT B
CUGAACUGAGUUUAAAAGGCACC	2247	32303	antisense	FLT1:364L21 siRNA (346C) inv stab10		CUUGACUCAAAUUUUUCCCGUTsT
UGAACUGAGUUUAAAAGGCACCC	2248	32304	antisense	FLT1:365L21 siRNA (347C) inv stab10		UUAGACUCAAAUUUUUCCCGUGTsT
GAACUGAGUUUAAAAGGCACCCA	2249	32305	antisense	FLT1:366L21 siRNA (348C) inv stab10		UGACUCAAAUUUUUCCCGUGTsT
ACUGAGUUUAAAAGGCACCCAGC	2250	32306	antisense	FLT1:368L21 siRNA (350C) inv stab10		ACUCAAAUUUUUCCCGUGGGUTsT
CUGAGUUUAAAAGGCACCCAGCA	2251	32307	antisense	FLT1:369L21 siRNA (351C) inv stab10		CUCAAAUUUUUCCCGUGGUCTsT
UGAGUUUAAAAGGCACCCAGCAC	2252	32308	antisense	FLT1:370L21 siRNA (352C) inv stab10		UCAAAUUUUUCCCGUGGUCGTsT
GAGUUUAAAAGGCACCCAGCACA	2253	32309	antisense	FLT1:371L21 siRNA (353C) inv stab10		CAAAUUUUUCCCGUGGUGCGUTsT
AACUGAGUUUAAAAGGCACCCAG	2009	32338	antisense	FLT1:367L21 siRNA (349C) stab10 3'-BrdU		GGGUGCCUUUUAAACUCAGXsT
AACUGAGUUUAAAAGGCACCCAG	2009	32718	antisense	FLT1:367L21 siRNA (349C) v1 5'p		pGGGUGCCUUUUAAACUC
AACUGAGUUUAAAAGGCACCCAG	2009	32719	antisense	FLT1:367L21 siRNA (349C) v2 5'p		GAGUUUAAAAG B
AAGCAAGGAGGGCCUCUGAUGGU	2012	32720	antisense	FLT1:2967L21 siRNA (2949C) v1 5'p		pGAGUUUAAAAG B
AAGCAAGGAGGGCCUCUGAUGGU	2012	32721	antisense	FLT1:2967L21 siRNA (2949C) v2 5'p		pCAUCAGAGGCCCUCCUUGC
AAGCAAGGAGGGCCUCUGAUGGU	2012	32722	antisense	FLT1:2967L21 siRNA (2949C) v3 5'p		AAGAGGGCCUCU B
CUGAACUGAGUUUAAAAGGCACC	2247	32748	antisense	FLT1:346U21 siRNA stab07 sense		pCAUCAGAGGCCCUCCU
UGAACUGAGUUUAAAAGGCACCC	2248	32749	antisense	FLT1:347U21 siRNA stab07 sense		AGAGGGCCUCUG B
GAACUGAGUUUAAAAGGCACCCA	2249	32750	antisense	FLT1:348U21 siRNA stab07 sense		B GAAcuGAGuuuAAAAAGGcATT B
						B AAcuGAGuuuAAAAAGGcATT B
						B AcuGAGuuuAAAAAGGcAccTT B

ACUGAGUUUAAAAGGCACCCAGC	2250	32751	FLT1:350U21 siRNA stab07 sense	B uGAGuuuAAAAGGcAcccATT B	2322
CUGAGUUUAAAAGGCACCCAGCA	2251	32752	FLT1:351U21 siRNA stab07 sense	B GAGuuuAAAAGGcAcccAGTT B	2323
UGAGUUUAAAAGGCACCCAGCAC	2252	32753	FLT1:352U21 siRNA stab07 sense	B AGuuuAAAAGGcAcccAGcTT B	2324
GAGUUUAAAAGGCACCCAGCACA	2253	32754	FLT1:353U21 siRNA stab07 sense	B GuuuAAAAGGcAcccAGcATT B	2325
CUGAACUGAGUUUAAAAGGCACC	2247	32755	FLT1:364L21 siRNA (346C) stab08 antisense	uGccuuuuAAA <u>cucAGuucTsT</u>	2326
UGAACUGAGUUUAAAAGGCACCCC	2248	32756	FLT1:365L21 siRNA (347C) stab08 antisense	GuGccuuuuAAA <u>cucAGuuTsT</u>	2327
GAACUGAGUUUAAAAGGCACCCA	2249	32757	FLT1:366L21 siRNA (348C) stab08 antisense	GGuGccuuuuAAA <u>cucAGuTsT</u>	2328
ACUGAGUUUAAAAGGCACCCAGC	2250	32758	FLT1:368L21 siRNA (350C) stab08 antisense	uGGGuGccuuuuAAA <u>cucATsT</u>	2329
CUGAGUUUAAAAGGCACCCAGCA	2251	32759	FLT1:369L21 siRNA (351C) stab08 antisense	cuGGGuGccuuuuAAA <u>cucTsT</u>	2330
UGAGUUUAAAAGGCACCCAGCAC	2252	32760	FLT1:370L21 siRNA (352C) stab08 antisense	GcuGGGuGccuuuuAAA <u>cucTsT</u>	2331
GAGUUUAAAAGGCACCCAGCACA	2253	32761	FLT1:371L21 siRNA (353C) stab08 antisense	uGcuGGGuGccuuuuAAA <u>cTsT</u>	2332
CUGAACUGAGUUUAAAAGGCACC	2247	32772	FLT1:346U21 siRNA inv stab07 sense	B AcGGAAAAuuuGAGucAAATT B	2333
UGAACUGAGUUUAAAAGGCACCC	2248	32773	FLT1:347U21 siRNA inv stab07 sense	B cAcGGAAAAuuuGAGucAAATT B	2334
GAACUGAGUUUAAAAGGCACCCA	2249	32774	FLT1:348U21 siRNA inv stab07 sense	B ccAcGGAAAAuuuGAGucATT B	2335
ACUGAGUUUAAAAGGCACCCAGC	2250	32775	FLT1:350U21 siRNA inv stab07 sense	B AcccAcGGAAAAuuuGAGuTT B	2336
CUGAGUUUAAAAGGCACCCAGCA	2251	32776	FLT1:351U21 siRNA inv stab07 sense	B GAcAcGGAAAAuuuGAGTT B	2337
UGAGUUUAAAAGGCACCCAGCAC	2252	32777	FLT1:352U21 siRNA inv stab07 sense	B cGAcAcGGAAAAuuuGATT B	2338
GAGUUUAAAAGGCACCCAGCACA	2253	32778	FLT1:353U21 siRNA inv stab07 sense	B AcGAcAcGGAAAAuuuGTT B	2339
CUGAACUGAGUUUAAAAGGCACC	2247	32779	FLT1:364L21 siRNA (346C) inv stab08 antisense	cuuGAcucAAAuuuu <u>uccGuTsT</u>	2340
UGAACUGAGUUUAAAAGGCACCCC	2248	32780	FLT1:365L21 siRNA (347C) inv stab08 antisense	uuGAcucAAAuuuu <u>uccGuTsT</u>	2341
GAACUGAGUUUAAAAGGCACCCA	2249	32781	FLT1:366L21 siRNA (348C) inv stab08 antisense	uGAcucAAAuuuu <u>uccGuGGTsT</u>	2342
ACUGAGUUUAAAAGGCACCCAGC	2250	32782	FLT1:368L21 siRNA (350C) inv stab08 antisense	AcucAAAuuuu <u>uccGuGGuTsT</u>	2343
CUGAGUUUAAAAGGCACCCAGCA	2251	32783	FLT1:369L21 siRNA (351C) inv stab08 antisense	cucAAAuuuu <u>uccGuGGGucTsT</u>	2344
UGAGUUUAAAAGGCACCCAGCAC	2252	32784	FLT1:370L21 siRNA (352C) inv stab08 antisense	ucAAAuuuu <u>uccGuGGGucTsT</u>	2345
GAGUUUAAAAGGCACCCAGCACA	2253	32785	FLT1:371L21 siRNA (353C) inv stab08 antisense	cAAAuuuu <u>uccGuGGGucGuTsT</u>	2346
AGTTTAAAAGGCACCCAGCACATC	2254	32805	FLT1:373L21 siRNA (354C) v1 5p antisense	pGUGCUGGGUGCCUUIUAAAA AGGACCCAGC B	2347
AGTTTAAAAGGCACCCAGCACATC	2254	32806	FLT1:373L21 siRNA (354C) v2 5p antisense	pGUGCUGGGUGCCUUIUAAAA GGCACCCAGC B	2348

AGTTAAAAGGCCACCCAGCACATC	2254	32807	FLT1:373L21 siRNA (354C) v3 5'p antisense	pGUGGUGGUGGCCUUAAAGGCACCCAGC B	2349
GCATATATATGATAAAGCATTCA	2255	32808	FLT1:1247L21 siRNA (1229C) v1 5'p antisense	pAAUGCUUUUAUCAUAUAU GAUAAAGC B	2350
GCATATATATGATAAAGCATTCA	2255	32809	FLT1:1247L21 siRNA (1229C) v2 5'p antisense	pAAUGCUUUUAUCAUAUAU GAUAAAGC B	2351
GCATATATATGATAAAGCATTCA	2255	32810	FLT1:1247L21 siRNA (1229C) v3 5'p antisense	pAAUGCUUUUAUCAUAU GAUAAAGC B	2352
GCATATATATGATAAAGCATTCA	2255	32811	FLT1:1247L21 siRNA (1229C) v4 5'p antisense	pAAUGCUUUUAUCAUAU GAUAAAGC B	2353
GCATATATATGATAAAGCATTCA	2255	32812	FLT1:1247L21 siRNA (1229C) v5 5'p antisense	pAAUGCUUUUAUCAUAU GAUAAAGCAUU B	2354
GCATATATATGATAAAGCATTCA	2255	32813	FLT1:1247L21 siRNA (1229C) v6 5'p antisense	pAAUGCUUUUAUCAUAU GAUAAAGCAUU B	2355
AACUGAGUUUAAAAAGGCACCCAG	2009	33056	FLT1:367L21 siRNA (349C) v3 5'p antisense	pGGGUGCCUUUUAAACUCAG GAGUUUAAAGG B	2356
AACUGAGUUUAAAAAGGCACCCAG	2009	33057	FLT1:367L21 siRNA (349C) v4 5'p antisense	pGGGUGCCUUUUAAACUC GAGUUUAAAGGC B	2357
AACUGAGUUUAAAAAGGCACCCAG	2009	33058	FLT1:367L21 siRNA (349C) v5 5'p antisense	pGGGUGCCUUUUAAACU AGUUUAAAGG B	2358
AACUGAGUUUAAAAAGGCACCCAG	2009	33059	FLT1:367L21 siRNA (349C) v6 5'p antisense	pGGGUGCCUUUUAAACU AGUUUAAAGGC B	2359
AACUGAGUUUAAAAAGGCACCCAG	2009	33060	FLT1:367L21 siRNA (349C) v7 5'p antisense	pGGGUGCCUUUUAAACU AGUUUAAAGGC B	2360
AACUGAGUUUAAAAAGGCACCCAG	2009	33061	FLT1:367L21 siRNA (349C) v8 5'p antisense	pGGGUGCCUUUUAAACU AGUUUAAAGGC B	2361
AACUGAGUUUAAAAAGGCACCCAG	2009	33062	FLT1:367L21 siRNA (349C) v9 5'p antisense	pGGGUGCCUUUUAAAC B	2362
AACUGAGUUUAAAAAGGCACCCAG	2009	33063	FLT1:367L21 siRNA (349C) v10 5'p antisense	pGGGUGCCUUUUAAAC GUUUUAAAGGC B	2363
AACUGAGUUUAAAAAGGCACCCAG	2009	33064	FLT1:367L21 siRNA (349C) v11 5'p antisense	pGGGUGCCUUUUAAAC GUUUUAAAGGC B	2364

VEGFR2

Target	Seq ID	COMPOUND#	Aliases	Sequence	Seq ID
UGACCUUGGAGCAUCUCAUCUGU	2001		KDR:3304U21 siRNA stab04 sense	B AccuuGGAGcAucucAucuTT B	2052
UCACCUUGUUUCCUGUUGGAGGA	2003		KDR:3894U21 siRNA stab04 sense	B AccuGuuuuccuGuAuGGAGTT B	2054
UGACCUUGGAGCAUCUCAUCUGU	2001		KDR:3322L21 siRNA (3304C) stab05 antisense	AGAuGAGAuGcuccAAAGGuTsT	2056
UCACCUUGUUUCCUGUUGGAGGA	2003		KDR:3912L21 siRNA (3894C) stab05 antisense	cuccAuAcAGGAAAcAGGuTsT	2058
UGACCUUGGAGCAUCUCAUCUGU	2001		KDR:3304U21 siRNA stab07 sense	B AccuuGGAGcAucucAucuTT B	2060

UCACCUUUUCCUGUAUGGAGGA	2003	32766	KDR:3894U21 siRNA stab07 sense KDR:3322L21 siRNA (3304C) stab11 antisense	B AccuGuuuuccuGuAuGGAGTT B	2062
UGACCUUGGAGCAUCUCAUCUGU	2001			AGAuGAGAGuGcuccAAGGuTsT	2064
UUUGAGCAUGGAAGAGGAUUCUG	2002		KDR:3872L21 siRNA (3854C) stab11 antisense	GAAuccucuccuAuGcucATsT	2065
UCACCUUUUCCUGUAUGGAGGA	2003		KDR:3912L21 siRNA (3894C) stab11 antisense	cuccAuAcAGGAAAcAGGuTsT	2066
GACAAACACAGCAGGAUUCAGUCA	2004		KDR:3966L21 siRNA (3948C) stab11 antisense	AcuGAuuccuGcuGuGuuGTsT	2067
UGUCCACUUAACCUAGGAGCAAG	2017	30785	KDR:3076U21 siRNA stab04 sense	B uccAcuuAccuGAGGAGcATT B	2205
UUUGAGCAUGGAAGAGGAUUCUG	2002	30786	KDR:3854U21 siRNA stab04 sense	B uGAGcAuGGAAAGAGGAuucTT B	2053
AUGGUUCUUGCCUCAGAGAGCU	2018	30787	KDR:4089U21 siRNA stab04 sense	B GGuucuuGccucAGAAAGAGTT B	2206
UCUGAAGGCUCAAACCAGACAAG	2019	30788	KDR:4191U21 siRNA stab04 sense	B uGAAAGGcucAAAaccAGAcATT B	2207
UGUCCACUUAACCUAGGAGCAAG	2017	30789	KDR:3094L21 siRNA (3076C) stab05 antisense	uGcucccAGGuAAAGuGGATsT	2208
UUUGAGCAUGGAAGAGGAUUCUG	2002	30790	KDR:3872L21 siRNA (3854C) stab05 antisense	GAAuccucuccuAuGcucATsT	2057
AUGGUUCUUGCCUCAGAGAGCU	2018	30791	KDR:4107L21 siRNA (4089C) stab05 antisense	cucuucUGAGGGcAAAGAAccTsT	2209
UCUGAAGGCUCAAACCAGACAAG	2019	30792	KDR:4209L21 siRNA (4191C) stab05 antisense	uGucuGGuuGAGcuccuATsT	2210
UGUCCACUUAACCUAGGAGCAAG	2017	31426	KDR:3076U21 siRNA sense	UCCACUUAACCUAGAGGAGcATT	2211
UUUGAGCAUGGAAGAGGAUUCUG	2002	31435	KDR:3854U21 siRNA sense	UGAGCAUGGAAGAGGAUUCITT	2045
AUGGUUCUUGCCUCAGAGAGCU	2018	31428	KDR:4089U21 siRNA sense	GGUUCUUGCCUCAGAAAGAGTT	2212
UCUGAAGGCUCAAACCAGACAAG	2019	31429	KDR:4191U21 siRNA sense	UGAAGGCUCAAACCAGACATT	2213
UGUCCACUUAACCUAGGAGCAAG	2017	31430	KDR:3094L21 siRNA (3076C) antisense	UGCUCUCAGGUAAUGUGGATT	2214
UUUGAGCAUGGAAGAGGAUUCUG	2002	31439	KDR:3872L21 siRNA (3854C) antisense	GAAUCCUCUUAUCCAUUGCUCATT	2049
AUGGUUCUUGCCUCAGAGAGCU	2018	31432	KDR:4107L21 siRNA (4089C) antisense	CUCUUCUGAGGGCAAGAACCTT	2215
UCUGAAGGCUCAAACCAGACAAG	2019	31433	KDR:4209L21 siRNA (4191C) antisense	UGUCUGGUUUGAGCCUUCATT	2216
UGACCUUGGAGCAUCUCAUCUGU	2001	31434	KDR:3304U21 siRNA sense	ACCUUGGAGCAUCUCAUCUTT	2044
UCACCUUUUCCUGUAUGGAGGA	2003	31436	KDR:3894U21 siRNA sense	ACCUGUUUCCUGUAUGGAGTT	2046
GACAAACACAGCAGGAUUCAGUCA	2004	31437	KDR:3948U21 siRNA sense	CAACACAGCAGGAUUCAGUTT	2047
UGACCUUGGAGCAUCUCAUCUGU	2001	31438	KDR:3322L21 siRNA (3304C) antisense	AGAUGAGAUUGCUCUCCAAAGUTT	2048
UCACCUUUUCCUGUAUGGAGGA	2003	31440	KDR:3912L21 siRNA (3894C) antisense	CUCCAUAACAGGAAACAGGUTT	2050
GACAAACACAGCAGGAUUCAGUCA	2004	31441	KDR:3966L21 siRNA (3948C) antisense	ACUGAUUCCUGCUGUGUUGTT	2051

GACAACACAGCAGGAAUCAGUCA	2004	31856	KDR:3948U21 siRNA stab04 sense KDR:3966L21 siRNA (3948C) stab05 antisense	B cAaAcAcAGcAGGAAuAcGuTT B	2055
GACAACACAGCAGGAAUCAGUCA	2004	31857		AcuGAuuccuGcuGuuGTsT	2059
UUUGAGCAUGGAAGAGGAUUCUG	2002	31858	KDR:3854U21 siRNA stab07 sense	B uGAGcAuGGAAAGAGGAuucTT B	2061
GACAACACAGCAGGAAUCAGUCA	2004	31859	KDR:3948U21 siRNA stab07 sense KDR:3872L21 siRNA (3854C) stab08 antisense	B cAaAcAcAGcAGGAAuAcGuTT B	2063
UUUGAGCAUGGAAGAGGAUUCUG	2002	31860		GAAuccuuccAuGcuATsT	2226
GACAACACAGCAGGAAUCAGUCA	2004	31861	KDR:3966L21 siRNA (3948C) stab08 antisense	AcuGAuuccuGcuGuuGTsT	2227
UUUGAGCAUGGAAGAGGAUUCUG	2002	31862	KDR:3854U21 siRNA stab09 sense	B uGAGCAUGGAAGAGGAUUC TT B	2228
GACAACACAGCAGGAAUCAGUCA	2004	31863	KDR:3948U21 siRNA stab09 sense KDR:3872L21 siRNA (3854C) stab10 antisense	B CAACACAGCAGGAAUCAGUTT B	2229
UUUGAGCAUGGAAGAGGAUUCUG	2002	31864		GAAUCCUCUCCAUCCGUCATsT	2230
GACAACACAGCAGGAAUCAGUCA	2004	31865	KDR:3966L21 siRNA (3948C) stab10 antisense	ACUGAUUCCUGCUGUGUUGTsT	2231
UUUGAGCAUGGAAGAGGAUUCUG	2002	31878	KDR:3854U21 siRNA inv stab04 sense	B cuuAGGAGAAAGGuAcGAGuTT B	2232
GACAACACAGCAGGAAUCAGUCA	2004	31879	KDR:3948U21 siRNA inv stab04 sense	B uGACuAAGGAcGAcAcAacTT B	2233
UUUGAGCAUGGAAGAGGAUUCUG	2002	31880	KDR:3872L21 siRNA (3854C) inv stab05 antisense	AcucGuAccuuccuAAAGTsT	2234
GACAACACAGCAGGAAUCAGUCA	2004	31881	KDR:3966L21 siRNA (3948C) inv stab05 antisense	GuuGuGucGuccuuAGucATsT	2235
UUUGAGCAUGGAAGAGGAUUCUG	2002	31882	KDR:3854U21 siRNA inv stab07 sense	B cuuAGGAGAAAGGuAcGAGuTT B	2236
GACAACACAGCAGGAAUCAGUCA	2004	31883	KDR:3948U21 siRNA inv stab07 sense	B uGACuAAGGAcGAcAcAacTT B	2237
UUUGAGCAUGGAAGAGGAUUCUG	2002	31884	KDR:3872L21 siRNA (3854C) inv stab08 antisense	AcucGuAccuuccuAAAGTsT	2238
GACAACACAGCAGGAAUCAGUCA	2004	31885	KDR:3966L21 siRNA (3948C) inv stab08 antisense	GuuGuGucGuccuuAGucATsT	2239
UUUGAGCAUGGAAGAGGAUUCUG	2002	31886	KDR:3854U21 siRNA inv stab09 sense	B CUUAGGAGAAGGUACGAGUTT B	2240
GACAACACAGCAGGAAUCAGUCA	2004	31887	KDR:3948U21 siRNA inv stab09 sense	B uGACUAAAGGACGACACAAC TT B	2241
UUUGAGCAUGGAAGAGGAUUCUG	2002	31888	KDR:3872L21 siRNA (3854C) inv stab10 antisense	ACUCGUACCUUUCUCCUAAAGTsT	2242
GACAACACAGCAGGAAUCAGUCA	2004	31889	KDR:3966L21 siRNA (3948C) inv stab10 antisense	GUUGUGUCGUCCUUAUGUCATsT	2243
CCUUAUGAUCCAGCAAAU	2256	32238	KDR:2764U21 siRNA sense	CCUUAUGAUCCAGCAAAU TT	2365
CUUAUGAUCCAGCAAAUG	2257	32239	KDR:2765U21 siRNA sense	CUUAUGAUCCAGCAAAU GTT	2366
UUAUGAUCCAGCAAAUGG	2258	32240	KDR:2766U21 siRNA sense	UUAUGAUCCAGCAAAU GGT	2367
UAUGAUCCAGCAAAUGGG	2259	32241	KDR:2767U21 siRNA sense	UAUGAUCCAGCAAAU GGGTT	2368

AUGAUGCCAGCAAAUGGGA	2260	32242	KDR:2768U21 siRNA sense	AUGAUGCCAGCAAAUGGGATT	2369
CAGACCAUGCUGGACUCGU	2261	32243	KDR:3712U21 siRNA sense	CAGACCAUGCUGGACUCGUTT	2370
AGACCAUGCUGGACUCUG	2262	32244	KDR:3713U21 siRNA sense	AGACCAUGCUGGACUCUGTT	2371
GACCAUGCUGGACUCUGG	2263	32245	KDR:3714U21 siRNA sense	GACCAUGCUGGACUCUGGTT	2372
ACCAUGCUGGACUCUGGC	2264	32246	KDR:3715U21 siRNA sense	ACCAUGCUGGACUCUGGCTT	2373
CCAUGCUGGACUCUGGCA	2265	32247	KDR:3716U21 siRNA sense	CCAUGCUGGACUCUGGCAATT	2374
CAGGAUGGCAAAAGACUACA	2266	32248	KDR:3811U21 siRNA sense	CAGGAUGGCAAAAGACUACATT	2375
AGGAUGGCAAAAGACUACAU	2267	32249	KDR:3812U21 siRNA sense	AGGAUGGCAAAAGACUACAUTT	2376
CCUUAUGAUGCCAGCAAAU	2256	32253	KDR:2782L21 siRNA (2764C) antisense	AUUUGCUGGCAUCAUAAGGTT	2377
CUUAUGAUGCCAGCAAAUG	2257	32254	KDR:2783L21 siRNA (2765C) antisense	CAUUUGCUGGCAUCAUAAGTT	2378
UUAUGAUGCCAGCAAAUGG	2258	32255	KDR:2784L21 siRNA (2766C) antisense	CCAUUUGCUGGCAUCAUAATT	2379
UAUGAUGCCAGCAAAUGGG	2259	32256	KDR:2785L21 siRNA (2767C) antisense	CCCAUUUGCUGGCAUCAUATT	2380
AUGAUGCCAGCAAAUGGGA	2260	32257	KDR:2786L21 siRNA (2768C) antisense	UCCCAUUUGCUGGCAUCAUATT	2381
CAGACCAUGCUGGACUCGU	2261	32258	KDR:3730L21 siRNA (3712C) antisense	AGCAGUCCAGCAUGGUCUGTT	2382
AGACCAUGCUGGACUCUG	2262	32259	KDR:3731L21 siRNA (3713C) antisense	CAGCAGUCCAGCAUGGUCUTT	2383
GACCAUGCUGGACUCUGG	2263	32260	KDR:3732L21 siRNA (3714C) antisense	CCAGCAGUCCAGCAUGGUCTT	2384
ACCAUGCUGGACUCUGGC	2264	32261	KDR:3733L21 siRNA (3715C) antisense	GCCAGCAGUCCAGCAUGGUTT	2385
CCAUGCUGGACUCUGGCA	2265	32262	KDR:3734L21 siRNA (3716C) antisense	UGCCAGCAGUCCAGCAUGGTT	2386
CAGGAUGGCAAAAGACUACA	2266	32263	KDR:3829L21 siRNA (3811C) antisense	UGUAGUCUUUGCCAUCUCCGTT	2387
AGGAUGGCAAAAGACUACAU	2267	32264	KDR:3830L21 siRNA (3812C) antisense	AUGUAGUCUUUGCCAUCUCCUTT	2388
UGACCUUGGAGCAUCUCAUCUGU	2001	32310	KDR:3304U21 siRNA stab09 sense	B ACCUUGGAGCAUCUCAUCUTT B	2389
UCACCUUGUUUCCUGUAUGGAGGA	2003	32311	KDR:3894U21 siRNA stab09 sense	B ACCUGUUUCCUGUAUGGAGTT B	2390
UGACCUUGGAGCAUCUCAUCUGU	2001	32312	KDR:3322L21 siRNA (3304C) stab10 antisense	AGAUGAGAUGCUCUCCAAGGUTsT	2391
UCACCUUGUUUCCUGUAUGGAGGA	2003	32313	KDR:3912L21 siRNA (3894C) stab10 antisense	CUCCAUACAGGAAACAGGUTsT	2392
UGACCUUGGAGCAUCUCAUCUGU	2001	32314	KDR:3304U21 siRNA inv stab09 sense	B UCUACUCUACGAGGUUCCATT B	2393
UCACCUUGUUUCCUGUAUGGAGGA	2003	32315	KDR:3894U21 siRNA inv stab09 sense	B GAGGUAUGUCCUUUGUCCATT B	2394
UGACCUUGGAGCAUCUCAUCUGU	2001	32316	KDR:3322L21 siRNA (3304C) inv	UGGAACCCUCGUAGAGUAGATsT	2395

UCACCGUUUCCUGUAGGAGGA	2003	32317	stab10 antisense	KDR:3912L21 siRNA (3894C) inv	UGGACAAAGGACAUACCUCTsT	2396
AACAGAAUUUCCUGGACAGCAA	2268	32762	stab10 antisense	KDR:828U21 siRNA stab07 sense	B cAGAAuuuccuGGGAcAcGcTT B	2397
UGGAGCAUCUCAGUCGUUACAGC	2269	32763	KDR:3310U21 siRNA stab07 sense	KDR:3310U21 siRNA stab07 sense	B GAGcAucucAucuGuuAcATT B	2398
CACGUUUUCAGAGUUGGGAAC	2270	32764	KDR:3758U21 siRNA stab07 sense	KDR:3758U21 siRNA stab07 sense	B cGUuuucAGAGuuGGUGGATT B	2399
CUCACCGUUUCCUGUAGGAGG	2271	32765	KDR:3893U21 siRNA stab07 sense	KDR:3893U21 siRNA stab07 sense	B cAccuGuuuuccuGuAuGGATT B	2400
AACAGAAUUUCCUGGACAGCAA	2268	32767	KDR:846L21 siRNA (828C) stab08 antisense	KDR:846L21 siRNA (828C) stab08 antisense	GcuGucccAGGAA <u>uuu</u> cUGTsT	2401
UGGAGCAUCUCAGUCGUUACAGC	2269	32768	KDR:3328L21 siRNA (3310C) stab08 antisense	KDR:3328L21 siRNA (3310C) stab08 antisense	uGuAAcAG <u>Au</u> GAG <u>Au</u> GcucTsT	2402
CACGUUUUCAGAGUUGGGAAC	2270	32769	KDR:3776L21 siRNA (3758C) stab08 antisense	KDR:3776L21 siRNA (3758C) stab08 antisense	uccAcAA <u>cucu</u> GAA <u>AA</u> cGTsT	2403
CUCACCGUUUCCUGUAGGAGG	2271	32770	KDR:3911L21 siRNA (3893C) stab08 antisense	KDR:3911L21 siRNA (3893C) stab08 antisense	ucc <u>Au</u> AcAGGAA <u>Ac</u> AGG <u>u</u> GTsT	2404
UCACCGUUUCCUGUAGGAGGA	2003	32771	KDR:3912L21 siRNA (3894C) stab08 antisense	KDR:3912L21 siRNA (3894C) stab08 antisense	cucc <u>Au</u> AcAGGAA <u>Ac</u> AGG <u>u</u> TsT	2405
AACAGAAUUUCCUGGACAGCAA	2268	32786	KDR:828U21 siRNA inv stab07 sense	KDR:828U21 siRNA inv stab07 sense	B cGAcAGGGuccuuuAAGAcTT B	2406
UGGAGCAUCUCAGUCGUUACAGC	2269	32787	KDR:3310U21 siRNA inv stab07 sense	KDR:3310U21 siRNA inv stab07 sense	B Ac <u>Auu</u> Guc <u>A</u> cuc <u>A</u> cAGAGTT B	2407
CACGUUUUCAGAGUUGGGAAC	2270	32788	KDR:3758U21 siRNA inv stab07 sense	KDR:3758U21 siRNA inv stab07 sense	B AGGuGGuuGAGAcuuuGcTT B	2408
CUCACCGUUUCCUGUAGGAGG	2271	32789	KDR:3893U21 siRNA inv stab07 sense	KDR:3893U21 siRNA inv stab07 sense	B AGGu <u>Au</u> GuccuuuGuccAcTT B	2409
UCACCGUUUCCUGUAGGAGGA	2003	32790	KDR:3894U21 siRNA inv stab07 sense	KDR:3894U21 siRNA inv stab07 sense	B GAGGu <u>Au</u> GuccuuuGuccATT B	2410
AACAGAAUUUCCUGGACAGCAA	2268	32791	KDR:846L21 siRNA (828C) inv stab08 antisense	KDR:846L21 siRNA (828C) inv stab08 antisense	GucuuAAAGGAGcccuGucGTsT	2411
UGGAGCAUCUCAGUCGUUACAGC	2269	32792	KDR:3328L21 siRNA (3310C) inv stab08 antisense	KDR:3328L21 siRNA (3310C) inv stab08 antisense	cucGuAGAG <u>u</u> AGAcAA <u>Au</u> GuTsT	2412
CACGUUUUCAGAGUUGGGAAC	2270	32793	KDR:3776L21 siRNA (3758C) inv stab08 antisense	KDR:3776L21 siRNA (3758C) inv stab08 antisense	GcAAAA <u>Guc</u> uAc <u>AA</u> ccuTsT	2413
CUCACCGUUUCCUGUAGGAGG	2271	32794	KDR:3911L21 siRNA (3893C) inv stab08 antisense	KDR:3911L21 siRNA (3893C) inv stab08 antisense	GuGGAcAAAGGAc <u>Au</u> AccuTsT	2414
UCACCGUUUCCUGUAGGAGGA	2003	32795	KDR:3912L21 siRNA (3894C) inv stab08 antisense	KDR:3912L21 siRNA (3894C) inv stab08 antisense	uGGAcAAAGGAc <u>Au</u> AccuTsT	2415
AACAGAAUUUCCUGGACAGCAA	2268	32958	KDR:828U21 siRNA stab09 sense	KDR:828U21 siRNA stab09 sense	B CAGAAUUUCCUGGACAGCCTT B	2416
UGGAGCAUCUCAGUCGUUACAGC	2269	32959	KDR:3310U21 siRNA stab09 sense	KDR:3310U21 siRNA stab09 sense	B GAGCAUCUCAGUCGUUACATT B	2417
CACGUUUUCAGAGUUGGGAAC	2270	32960	KDR:3758U21 siRNA stab09 sense	KDR:3758U21 siRNA stab09 sense	B CGUUUUCAGAGUUGGUGGATT B	2418
CUCACCGUUUCCUGUAGGAGG	2271	32961	KDR:3893U21 siRNA stab09 sense	KDR:3893U21 siRNA stab09 sense	B CACCUGUUUCCUGUAUGGATT B	2419
AACAGAAUUUCCUGGACAGCAA	2268	32963	KDR:846L21 siRNA (828C) stab10 antisense	KDR:846L21 siRNA (828C) stab10 antisense	GCUGUCCCAGGAA <u>uu</u> UCUGTsT	2420
UGGAGCAUCUCAGUCGUUACAGC	2269	32964	KDR:3328L21 siRNA (3310C) stab10 antisense	KDR:3328L21 siRNA (3310C) stab10 antisense	UGUAACAGAGAGAGUGCUCTsT	2421

			antisense			
CACGUUUUCAGAGUUGGGAAC	2270	32965	KDR:3776L21 siRNA (3758C) stab10 antisense	UCCACCAACUCUGAAAAACGTsT	2422	
CUCACCCUGUUUCCUGUAUGGAGG	2271	32966	KDR:3911L21 siRNA (3893C) stab10 antisense	UCCAUACAGGAAACAGGUGTsT	2423	
AACAGAAUUUCCUGGGACAGCAA	2268	32988	KDR:828U21 siRNA inv stab09 sense	B CGACAGGGUCCUUUAAAGACTT B	2424	
UGGAGCAUCUCAUCUGUACAGC	2269	32989	KDR:3310U21 siRNA inv stab09 sense	B ACAUUGUCUACUCUACGAGTT B	2425	
CACGUUUUCAGAGUUGGGAAC	2270	32990	KDR:3758U21 siRNA inv stab09 sense	B AGGUGGUUGAGACUUUUGCTT B	2426	
CUCACCCUGUUUCCUGUAUGGAGG	2271	32991	KDR:3893U21 siRNA inv stab09 sense	B AGGU AUGUCCUUUGUCCACTT B	2427	
AACAGAAUUUCCUGGGACAGCAA	2268	32993	KDR:846L21 siRNA (828C) inv stab10 antisense	GUCUUAAAGGACCCUGUCGTsT	2428	
UGGAGCAUCUCAUCUGUACAGC	2269	32994	KDR:3328L21 siRNA (3310C) inv stab10 antisense	CUCGUAGAGUAGACAAUGUTsT	2429	
CACGUUUUCAGAGUUGGGAAC	2270	32995	KDR:3776L21 siRNA (3758C) inv stab10 antisense	GCAAAAGUCUCAACCACCUtsT	2430	
CUCACCCUGUUUCCUGUAUGGAGG	2271	32996	KDR:3911L21 siRNA (3893C) inv stab10 antisense	GUGGACAAAGGACAUACCUtsT	2431	

VEGFR3

Target	Seq ID	COMPOUND#	Aliases	Sequence	Seq ID
AGCACUGCCACAAGAAAGUACCUG	2005	31904	FLT4:2011U21 siRNA sense	CACUGCCACAAGAAAGUACCTT	2068
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3921U21 siRNA sense	GAAGCAGAGAGAGAGAAAGGTT	2069
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4038U21 siRNA sense	AGAGGAACCCAGGAGGACAATT	2070
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4054U21 siRNA sense	CAAGAGGAGCAUGAAAGUGTT	2071
AGCACUGCCACAAGAAAGUACCUG	2005	31908	FLT4:2029L21 siRNA (2011C) antisense	GGUACUUCUUGUGGCAGUGTT	2072
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3939L21 siRNA (3921C) antisense	CCUUCUCUCUCUCUGCUUCTT	2073
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4056L21 siRNA (4038C) antisense	UUGUCCUCCUGGUUCCUCUTT	2074
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4072L21 siRNA (4054C) antisense	CACUUUCAUGCUCCUCUUGTT	2075
AGCACUGCCACAAGAAAGUACCUG	2005		FLT4:2011U21 siRNA stab04 sense	B cAcuGccAcAAGAAAGuAccTT B	2076
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3921U21 siRNA stab04 sense	B GAAGcAGAGAGAGAGAAAGGTT B	2077
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4038U21 siRNA stab04 sense	B AGAGGAaccAGGAGGAcAAATT B	2078
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4054U21 siRNA stab04 sense	B cAAGAGGAGcAuGAAAAGuGTT B	2079
AGCACUGCCACAAGAAAGUACCUG	2005		FLT4:2029L21 siRNA (2011C) stab05 antisense	GGuAcuucuuGuGGcAGuGTsT	2080
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3939L21 siRNA (3921C) stab05 antisense	ccuucucucucucuGcuucTsT	2081
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4056L21 siRNA (4038C) stab05 antisense	uuGuccuuccuGGuuccucuTsT	2082
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4072L21 siRNA (4054C) stab05 antisense	cAcuuucAuGcuuccucuTsT	2083
AGCACUGCCACAAGAAAGUACCUG	2005		FLT4:2011U21 siRNA stab07 sense	B cAcuGccAcAAAGAAAGuAccTT B	2084
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3921U21 siRNA stab07 sense	B GAAGcAGAGAGAGAGAAAGGTT B	2085
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4038U21 siRNA stab07 sense	B AGAGGAaccAGGAGGAcAAATT B	2086
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4054U21 siRNA stab07 sense	B cAAGAGGAGcAuGAAAAGuGTT B	2087
AGCACUGCCACAAGAAAGUACCUG	2005		FLT4:2029L21 siRNA (2011C) stab11 antisense	GGuAcuucuuGuGGcAGuGTsT	2088
CUGAAGCAGAGAGAGAGAAAGGCA	2006		FLT4:3939L21 siRNA (3921C) stab11 antisense	ccuucucucucucuGcuucTsT	2089
AAAGAGGAACCCAGGAGGACAAGA	2007		FLT4:4056L21 siRNA (4038C) stab11 antisense	uuGuccuuccuGGuuccucuTsT	2090
GACAAGAGGAGCAUGAAAGUGGA	2008		FLT4:4072L21 siRNA (4054C) stab11 antisense	cAcuuucAuGcuuccucuTsT	2091

ACUUCUAUGUGACCACCAUCCCC	2272	31902	FLT4:1666U21 siRNA sense	UUCUAUGUGACCACCAUCCCTT	2432
CAAGCACUGCCACAAAGAGUACC	2273	31903	FLT4:2009U21 siRNA sense	AGCACUGCCACAAAGAGUATT	2433
AGUACGGCAACCUCUCCAAACUUC	2274	31905	FLT4:2815U21 siRNA sense	UACGGCAACCUCUCCAAACUUTT	2434
ACUUCUAUGUGACCACCAUCCCC	2272	31906	FLT4:1684L21 siRNA (1666C) antisense	GGAUGGGUGGUCACAUAGAATT	2435
CAAGCACUGCCACAAAGAGUACC	2273	31907	FLT4:2027L21 siRNA (2009C) antisense	UACUUCUUUGUGGCAGUGCUTT	2436
AGUACGGCAACCUCUCCAAACUUC	2274	31909	FLT4:2833L21 siRNA (2815C) antisense	AGUUGGAGAGGUUGCCGUATT	2437

Uppercase = ribonucleotide
u,c = 2'-deoxy-2'-fluoro U,C
T = thymidine
B = inverted deoxy abasic
s = phosphorothioate linkage
A = deoxy Adenosine
G = deoxy Guanosine
A = 2'-O-methyl Adenosine
G = 2'-O-methyl Guanosine
X= nitroindole universal base
Z= nitropyrole universal base
Y= 3',3'-inverted thymidine
M= glyceryl
N= 3'-O-methyl uridine
P= L-thymidine
Q= L-uridine
R= 5-bromo-deoxy-uridine
Z = sbL: symmetrical
bifunctional linker
H = chol2: capped Cholesterol
TEG

Table IV

Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	Purine	cap	p=S	Strand
“Stab 1”	Ribo	Ribo	-	5 at 5'-end 1 at 3'-end	S/AS
“Stab 2”	Ribo	Ribo	-	All linkages	Usually AS
“Stab 3”	2'-fluoro	Ribo	-	4 at 5'-end 4 at 3'-end	Usually S
“Stab 4”	2'-fluoro	Ribo	5' and 3'-ends	-	Usually S
“Stab 5”	2'-fluoro	Ribo	-	1 at 3'-end	Usually AS
“Stab 6”	2'-O-Methyl	Ribo	5' and 3'-ends	-	Usually S
“Stab 7”	2'-fluoro	2'-deoxy	5' and 3'-ends	-	Usually S
“Stab 8”	2'-fluoro	2'-O-Methyl	-	1 at 3'-end	Usually AS
“Stab 9”	Ribo	Ribo	5' and 3'-ends	-	Usually S
“Stab 10”	Ribo	Ribo	-	1 at 3'-end	Usually AS
“Stab 11”	2'-fluoro	2'-deoxy	-	1 at 3'-end	Usually AS
“Stab 12”	2'-fluoro	LNA	5' and 3'-ends		Usually S
“Stab 13”	2'-fluoro	LNA		1 at 3'-end	Usually AS
“Stab 14”	2'-fluoro	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually AS
“Stab 15”	2'-deoxy	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually AS
“Stab 16	Ribo	2'-O-Methyl	5' and 3'-ends		Usually S
“Stab 17”	2'-O-Methyl	2'-O-Methyl	5' and 3'-ends		Usually S

"Stab 18"	2' -fluoro	2'-O-Methyl	ends 5' and 3' - ends	1 at 3' -end	Usually S	

CAP = any terminal cap, see for example **Figure 10**.

All Stab 1-18 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 1-18 chemistries typically comprise 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V**A. 2.5 μ mol Synthesis Cycle ABI 394 Instrument**

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 μ L	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μ L	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 μ L	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 μ L	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μ L	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 μ L	5 sec	5 sec	5 sec
TCA	700	732 μ L	10 sec	10 sec	10 sec
Iodine	20.6	244 μ L	15 sec	15 sec	15 sec
Beaucage	7.7	232 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μ mol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O- methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μ L	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μ L	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μ L	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μ L	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 μ L	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μ L	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μ L	NA	NA	NA

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- Wait time does not include contact time during delivery.
 - Tandem synthesis utilizes double coupling of linker molecule